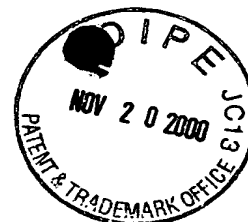


1
SEQUENCE LISTING



#9
RECEIVED

NOV 24 2000

TECH CENTER 1600/2300

RECEIVED

NOV 27 2000

TECH CENTER 1600/2300

<110> Galdes, Alphonse
Mahanthappa, Nagesh

<120> METHODS AND COMPOSITIONS FOR TREATING DISORDERS INVOLVING
EXCITOTOXICITY

<130> BIV-069.02

<140> 09/325,602

<141> 1999-06-03

<150> 09/238,243

<151> 1999-01-27

<160> 32

<170> PatentIn Ver. 2.1

<210> 1

<211> 1277

<212> DNA

<213> Gallus sp.

<220>

<221> CDS

<222> (1)..(1275)

<400> 1

atg gtc gaa atg ctg ctg ttg aca aga att ctc ttg gtg ggc ttc atc	48
Met Val Glu Met Leu Leu Leu Thr Arg Ile Leu Leu Val Gly Phe Ile	
1 5 10 15	
tgc gct ctt tta gtc tcc tct ggg ctg act tgt gga cca ggc agg ggc	96
Cys Ala Leu Leu Val Ser Ser Gly Leu Thr Cys Gly Pro Gly Arg Gly	
20 25 30	
att gga aaa agg agg cac ccc aaa aag ctg acc ccg tta gcc tat aag	144
Ile Gly Lys Arg Arg His Pro Lys Lys Leu Thr Pro Leu Ala Tyr Lys	
35 40 45	
cag ttt att ccc aat gtg gca gag aag acc cta ggg gcc agt gga aga	192
Gln Phe Ile Pro Asn Val Ala Glu Lys Thr Leu Gly Ala Ser Gly Arg	
50 55 60	
tat gaa ggg aag atc aca aga aac tcc gag aga ttt aaa gaa cta acc	240
Tyr Glu Gly Lys Ile Thr Arg Asn Ser Glu Arg Phe Lys Glu Leu Thr	
65 70 75 80	
cca aat tac aac cct gac att att ttt aag gat gaa gag aac acg gga	288
Pro Asn Tyr Asn Pro Asp Ile Ile Phe Lys Asp Glu Glu Asn Thr Gly	
85 90 95	
gct gac aga ctg atg act cag cgc tgc aag gac aag ctg aat gcc ctg	336
Ala Asp Arg Leu Met Thr Gln Arg Cys Lys Asp Lys Leu Asn Ala Leu	
100 105 110	

gcg atc tcg gtg atg aac cag tgg ccc ggg gtg aag ctg cgg gtg acc	384
Ala Ile Ser Val Met Asn Gln Trp Pro Gly Val Lys Leu Arg Val Thr	
115 120 125	
gag ggc tgg gac gag gat ggc cat cac tcc gag gaa tcg ctg cac tac	432
Glu Gly Trp Asp Glu Asp Gly His His Ser Glu Glu Ser Leu His Tyr	
130 135 140	
gag ggt cgc gcc gtg gac atc acc acg tcg gat cgg gac cgc agc aag	480
Glu Gly Arg Ala Val Asp Ile Thr Thr Ser Asp Arg Asp Arg Ser Lys	
145 150 155 160	
tac gga atg ctg gcc cgc ctc gcc gtc gag gcc ggc ttc gac tgg gtc	528
Tyr Gly Met Leu Ala Arg Leu Ala Val Glu Ala Gly Phe Asp Trp Val	
165 170 175	
tac tac gag tcc aag gcg cac atc cac tgc tcc gtc aaa gca gaa aac	576
Tyr Tyr Glu Ser Lys Ala His Ile His Cys Ser Val Lys Ala Glu Asn	
180 185 190	
tca gtg gca gcg aaa tca gga ggc tgc ttc cct ggc tca gcc aca gtg	624
Ser Val Ala Ala Lys Ser Gly Gly Cys Phe Pro Gly Ser Ala Thr Val	
195 200 205	
cac ctg gag cat gga ggc acc aag ctg gtg aag gac ctg agc cct ggg	672
His Leu Glu His Gly Gly Thr Lys Leu Val Lys Asp Leu Ser Pro Gly	
210 215 220	
gac cgc gtg ctg gct gct gac gcg gac ggc cgg ctg ctc tac agt gac	720
Asp Arg Val Leu Ala Ala Asp Ala Asp Gly Arg Leu Leu Tyr Ser Asp	
225 230 235 240	
ttc ctc acc ttc ctc gac cgg atg gac agc tcc cga aag ctc ttc tac	768
Phe Leu Thr Phe Leu Asp Arg Met Asp Ser Ser Arg Lys Leu Phe Tyr	
245 250 255	
gtc atc gag acg cgg cag ccc cgg gcc cgg ctg cta ctg acg gcg gcc	816
Val Ile Glu Thr Arg Gln Pro Arg Ala Arg Leu Leu Leu Thr Ala Ala	
260 265 270	
cac ctg ctc ttt gtg gcc ccc cag cac aac cag tcg gag gcc aca ggg	864
His Leu Leu Phe Val Ala Pro Gln His Asn Gln Ser Glu Ala Thr Gly	
275 280 285	
tcc acc agt ggc cag gcg ctc ttc gcc agc aac gtg aag cct ggc caa	912
Ser Thr Ser Gly Gln Ala Leu Phe Ala Ser Asn Val Lys Pro Gly Gln	
290 295 300	
cgt gtc tat gtg ctg ggc gag ggc ggg cag cag ctg ctg ccg gcg tct	960
Arg Val Tyr Val Leu Gly Glu Gly Gly Gln Gln Leu Leu Pro Ala Ser	
305 310 315 320	
gtc cac agc gtc tca ttg cgg gag gag gcg tcc gga gcc tac gcc cca	1008
Val His Ser Val Ser Leu Arg Glu Glu Ala Ser Gly Ala Tyr Ala Pro	
325 330 335	

ctc acc gcc cag ggc acc atc ctc atc aac cgg gtg ttg gcc tcc tgc	1056
Leu Thr Ala Gln Gly Thr Ile Leu Ile Asn Arg Val Leu Ala Ser Cys	
340 345 350	
tac gcc gtc atc gag gag cac agt tgg gcc cat tgg gcc ttc gca cca	1104
Tyr Ala Val Ile Glu Glu His Ser Trp Ala His Trp Ala Phe Ala Pro	
355 360 365	
ttc cgc ttg gct cag ggg ctg ctg gcc gcc ctc tgc cca gat ggg gcc	1152
Phe Arg Leu Ala Gln Gly Leu Leu Ala Ala Leu Cys Pro Asp Gly Ala	
370 375 380	
atc cct act gcc gcc acc acc acc act ggc atc cat tgg tac tca cgg	1200
Ile Pro Thr Ala Ala Thr Thr Thr Thr Gly Ile His Trp Tyr Ser Arg	
385 390 395 400	
ctc ctc tac cgc atc ggc agc tgg gtg ctg gat ggt gac gcg ctg cat	1248
Leu Leu Tyr Arg Ile Gly Ser Trp Val Leu Asp Gly Asp Ala Leu His	
405 410 415	
ccg ctg ggc atg gtg gca ccg gcc agc tg	1277
Pro Leu Gly Met Val Ala Pro Ala Ser	
420 425	
<210> 2	
<211> 1190	
<212> DNA	
<213> Murine sp.	
<220>	
<221> CDS	
<222> (1)..(1188)	
<400> 2	
atg gct ctg ccg gcc agt ctg ttg ccc ctg tgc tgc ttg gca ctc ttg	48
Met Ala Leu Pro Ala Ser Leu Leu Pro Leu Cys Cys Leu Ala Leu Leu	
1 5 10 15	
gca cta tct gcc cag agc tgc ggg ccg ggc cga gga ccg gtt ggc cgg	96
Ala Leu Ser Ala Gln Ser Cys Gly Pro Gly Arg Gly Pro Val Gly Arg	
20 25 30	
cgg cgt tat gtg cgc aag caa ctt gtg cct ctg cta tac aag cag ttt	144
Arg Arg Tyr Val Arg Lys Gln Leu Val Pro Leu Leu Tyr Lys Gln Phe	
35 40 45	
gtg ccc agt atg ccc gag cgg acc ctg ggc gcg agt ggg cca gcg gag	192
Val Pro Ser Met Pro Glu Arg Thr Leu Gly Ala Ser Gly Pro Ala Glu	
50 55 60	
ggg agg gta aca agg ggg tcg gag cgc ttc cgg gac ctc gta ccc aac	240
Gly Arg Val Thr Arg Gly Ser Glu Arg Phe Arg Asp Leu Val Pro Asn	
65 70 75 80	
tac aac ccc gac ata atc ttc aag gat gag gag aac agc ggc gca gac	288
Tyr Asn Pro Asp Ile Ile Phe Lys Asp Glu Glu Asn Ser Gly Ala Asp	
85 90 95	

NOV 24 2000

cgc ctg atg aca gag cgt tgc aaa gag cgg gtg aac gct cta gcc atc Arg Leu Met Thr Glu Arg Cys Lys Glu Arg Val Asn Ala Leu Ala Ile 100 105 110	336
gcg gtg atg aac atg tgg ccc gga gta cgc cta cgt gtg act gaa ggc Ala Val Met Asn Met Trp Pro Gly Val Arg Leu Arg Val Thr Glu Gly 115 120 125	384
tgg gac gag gac ggc cac cac gca cag gat tca ctc cac tac gaa ggc Trp Asp Glu Asp Gly His His Ala Gln Asp Ser Leu His Tyr Glu Gly 130 135 140	432
cgt gcc ttg gac atc acc acg tct gac cgt gac cgt aat aag tat ggt Arg Ala Leu Asp Ile Thr Thr Ser Asp Arg Asp Arg Asn Lys Tyr Gly 145 150 155 160	480
ttg ttg gcg cgc cta gct gtg gaa gcc gga ttc gac tgg gtc tac tac Leu Leu Ala Arg Leu Ala Val Glu Ala Gly Phe Asp Trp Val Tyr Tyr 165 170 175	528
gag tcc cgc aac cac atc cac gta tcg gtc aaa gct gat aac tca ctg Glu Ser Arg Asn His Ile His Val Ser Val Lys Ala Asp Asn Ser Leu 180 185 190	576
gcg gtc cga gcc gga ggc tgc ttt ccg gga aat gcc acg gtg cgc ttg Ala Val Arg Ala Gly Gly Cys Phe Pro Gly Asn Ala Thr Val Arg Leu 195 200 205	624
cgg agc ggc gaa cgg aag ggg ctg agg gaa cta cat cgt ggt gac tgg Arg Ser Gly Glu Arg Lys Gly Leu Arg Glu Leu His Arg Gly Asp Trp 210 215 220	672
gta ctg gcc gct gat gca gcg ggc cga gtg gta ccc acg cca gtg ctg Val Leu Ala Ala Asp Ala Ala Gly Arg Val Val Pro Thr Pro Val Leu 225 230 235 240	720
ctc ttc ctg gac cgg gat ctg cag cgc cgc gcc tcg ttc gtg gct gtg Leu Phe Leu Asp Arg Asp Leu Gln Arg Arg Ala Ser Phe Val Ala Val 245 250 255	768
gag acc gag cgg cct ccg cgc aaa ctg ttg ctc aca ccc tgg cat ctg Glu Thr Glu Arg Pro Pro Arg Lys Leu Leu Leu Thr Pro Trp His Leu 260 265 270	816
gtg ttc gct gct cgc ggg cca gcg cct gct cca ggt gac ttt gca ccg Val Phe Ala Ala Arg Gly Pro Ala Pro Ala Pro Gly Asp Phe Ala Pro 275 280 285	864
gtg ttc gcg cgc cgc tta cgt gct ggc gac tcg gtg ctg gct ccc ggc Val Phe Ala Arg Arg Leu Arg Ala Gly Asp Ser Val Leu Ala Pro Gly 290 295 300	912
ggg gac gcg ctc cag ccg gcg cgc gta gcc cgc gtg gcg cgc gag gaa Gly Asp Ala Leu Gln Pro Ala Arg Val Ala Arg Val Ala Arg Glu Glu 305 310 315 320	960

TECH CENTER 1600/2800

gcc gtg ggc gtg ttc gca ccg ctc act gcg cac ggg acg ctg ctg gtc	1008
Ala Val Gly Val Phe Ala Pro Leu Thr Ala His Gly Thr Leu Leu Val	
325 330 335	
aac gac gtc ctc gcc tcc tgc tac gcg gtt cta gag agt cac cag tgg	1056
Asn Asp Val Leu Ala Ser Cys Tyr Ala Val Leu Glu Ser His Gln Trp	
340 345 350	
gcc cac cgc gcc ttc gcc cct ttg cgg ctg ctg cac gcg ctc ggg gct	1104
Ala His Arg Ala Phe Ala Pro Leu Arg Leu Leu His Ala Leu Gly Ala	
355 360 365	
ctg ctc cct ggg ggt gca gtc cag ccg act ggc atg cat tgg tac tct	1152
Leu Leu Pro Gly Gly Ala Val Gln Pro Thr Gly Met His Trp Tyr Ser	
370 375 380	
cgc ctc ctt tac cgc ttg gcc gag gag tta atg ggc tg	1190
Arg Leu Leu Tyr Arg Leu Ala Glu Glu Leu Met Gly	
385 390 395	
<210> 3	
<211> 1281	
<212> DNA	
<213> Murine sp.	
<220>	
<221> CDS	
<222> (1)..(1233)	
<400> 3	
atg tct ccc gcc tgg ctc cgg ccc cga ctg cgg ttc tgt ctg ttc ctg	48
Met Ser Pro Ala Trp Leu Arg Pro Arg Leu Arg Phe Cys Leu Phe Leu	
1 5 10 15	
ctg ctg ctg ctt ctg gtg ccg gcg gcg cgg ggc tgc ggg ccg ggc cgg	96
Leu Leu Leu Leu Leu Val Pro Ala Ala Arg Gly Cys Gly Pro Gly Arg	
20 25 30	
gtg gtg ggc agc cgc cgg agg ccg cct cgc aag ctc gtg cct ctt gcc	144
Val Val Gly Ser Arg Arg Arg Pro Pro Arg Lys Leu Val Pro Leu Ala	
35 40 45	
tac aag cag ttc agc ccc aac gtg ccg gag aag acc ctg ggc gcc agc	192
Tyr Lys Gln Phe Ser Pro Asn Val Pro Glu Lys Thr Leu Gly Ala Ser	
50 55 60	
ggg cgc tac gaa ggc aag atc gcg cgc agc tct gag cgc ttc aaa gag	240
Gly Arg Tyr Glu Gly Lys Ile Ala Arg Ser Ser Glu Arg Phe Lys Glu	
65 70 75 80	
ctc acc ccc aac tac aat ccc gac atc atc ttc aag gac gag gag aac	288
Leu Thr Pro Asn Tyr Asn Pro Asp Ile Ile Phe Lys Asp Glu Glu Asn	
85 90 95	
acg ggt gcc gac cgc ctc atg acc cag gcg tgc aag gac cgt ctg aac	336
Thr Gly Ala Asp Arg Leu Met Thr Gln Arg Cys Lys Asp Arg Leu Asn	
100 105 110	

tca	ctg	gcc	atc	tct	gtc	atg	aac	cag	tgg	cct	ggg	gtg	aaa	ctg	cgg	384
Ser	Leu	Ala	Ile	Ser	Val	Met	Asn	Gln	Trp	Pro	Gly	Val	Lys	Leu	Arg	
		115					120					125				
gtg	acc	gaa	ggc	cgg	gat	gaa	gat	ggc	cat	cac	tca	gag	gag	tct	tta	432
Val	Thr	Glu	Gly	Arg	Asp	Glu	Asp	Gly	His	His	Ser	Glu	Glu	Ser	Leu	
	130					135					140					
cac	tat	gag	ggc	cgc	gcg	gtg	gat	atc	acc	acc	tca	gac	cgt	gac	cga	480
His	Tyr	Glu	Gly	Arg	Ala	Val	Asp	Ile	Thr	Thr	Ser	Asp	Arg	Asp	Arg	
145					150					155					160	
aat	aag	tat	gga	ctg	ctg	gcg	cgc	tta	gca	gtg	gag	gcc	ggc	ttc	gac	528
Asn	Lys	Tyr	Gly	Leu	Leu	Ala	Arg	Leu	Ala	Val	Glu	Ala	Gly	Phe	Asp	
			165					170						175		
tgg	gtg	tat	tac	gag	tcc	aag	gcc	cac	gtg	cat	tgc	tct	gtc	aag	tct	576
Trp	Val	Tyr	Tyr	Glu	Ser	Lys	Ala	His	Val	His	Cys	Ser	Val	Lys	Ser	
		180					185						190			
gag	cat	tcg	gcc	gct	gcc	aag	aca	ggg	ggc	tgc	ttt	cct	gcc	gga	gcc	624
Glu	His	Ser	Ala	Ala	Ala	Lys	Thr	Gly	Gly	Cys	Phe	Pro	Ala	Gly	Ala	
		195					200					205				
cag	gtg	cgc	cta	gag	aac	ggg	gag	cgt	gtg	gcc	ctg	tca	gct	gta	aag	672
Gln	Val	Arg	Leu	Glu	Asn	Gly	Glu	Arg	Val	Ala	Leu	Ser	Ala	Val	Lys	
	210					215					220					
cca	gga	gac	cgg	gtg	ctg	gcc	atg	ggg	gag	gat	ggg	acc	ccc	acc	ttc	720
Pro	Gly	Asp	Arg	Val	Leu	Ala	Met	Gly	Glu	Asp	Gly	Thr	Pro	Thr	Phe	
225					230					235					240	
agt	gat	gtg	ctt	att	ttc	ctg	gac	cgc	gag	cca	aac	cgg	ctg	aga	gct	768
Ser	Asp	Val	Leu	Ile	Phe	Leu	Asp	Arg	Glu	Pro	Asn	Arg	Leu	Arg	Ala	
			245						250					255		
ttc	cag	gtc	atc	gag	act	cag	gat	cct	ccg	cgt	cgg	ctg	gcg	ctc	acg	816
Phe	Gln	Val	Ile	Glu	Thr	Gln	Asp	Pro	Pro	Arg	Arg	Leu	Ala	Leu	Thr	
		260						265					270			
cct	gcc	cac	ctg	ctc	ttc	att	gcg	gac	aat	cat	aca	gaa	cca	gca	gcc	864
Pro	Ala	His	Leu	Leu	Phe	Ile	Ala	Asp	Asn	His	Thr	Glu	Pro	Ala	Ala	
		275					280					285				
cac	ttc	cgg	gcc	aca	ttt	gcc	agc	cat	gtg	caa	cca	ggc	caa	tat	gtg	912
His	Phe	Arg	Ala	Thr	Phe	Ala	Ser	His	Val	Gln	Pro	Gly	Gln	Tyr	Val	
	290					295				300						
ctg	gta	tca	ggg	gta	cca	ggc	ctc	cag	cct	gct	cgg	gtg	gca	gct	gtc	960
Leu	Val	Ser	Gly	Val	Pro	Gly	Leu	Gln	Pro	Ala	Arg	Val	Ala	Ala	Val	
305					310					315					320	
tcc	acc	cac	gtg	gcc	ctt	ggg	tcc	tat	gct	cct	ctc	aca	agg	cat	ggg	1008
Ser	Thr	His	Val	Ala	Leu	Gly	Ser	Tyr	Ala	Pro	Leu	Thr	Arg	His	Gly	
			325						330					335		

aca ctt gtg gtg gag gat gtg gtg gcc tcc tgc ttt gca gct gtg gct 1056
 Thr Leu Val Val Glu Asp Val Val Ala Ser Cys Phe Ala Ala Val Ala
 340 345 350

gac cac cat ctg gct cag ttg gcc ttc tgg ccc ctg cga ctg ttt ccc 1104
 Asp His His Leu Ala Gln Leu Ala Phe Trp Pro Leu Arg Leu Phe Pro
 355 360 365

agt ttg gca tgg ggc agc tgg acc cca agt gag ggt gtt cac tcc tac 1152
 Ser Leu Ala Trp Gly Ser Trp Thr Pro Ser Glu Gly Val His Ser Tyr
 370 375 380

cct cag atg ctc tac cgc ctg ggg cgt ctc ttg cta gaa gag agc acc 1200
 Pro Gln Met Leu Tyr Arg Leu Gly Arg Leu Leu Leu Glu Glu Ser Thr
 385 390 395 400

ttc cat cca ctg ggc atg tct ggg gca gga agc tgaagggact ctaaccactg 1253
 Phe His Pro Leu Gly Met Ser Gly Ala Gly Ser
 405 410

ccctcctgga actgctgtgc gtggatcc 1281

<210> 4
 <211> 1313
 <212> DNA
 <213> Murine sp.

<220>
 <221> CDS
 <222> (1)..(1311)

<400> 4
 atg ctg ctg ctg ctg gcc aga tgt ttt ctg gtg atc ctt gct tcc tcg 48
 Met Leu Leu Leu Leu Ala Arg Cys Phe Leu Val Ile Leu Ala Ser Ser
 1 5 10 15

ctg ctg gtg tgc ccc ggg ctg gcc tgt ggg ccc ggc agg ggg ttt gga 96
 Leu Leu Val Cys Pro Gly Leu Ala Cys Gly Pro Gly Arg Gly Phe Gly
 20 25 30

aag agg cgg cac ccc aaa aag ctg acc cct tta gcc tac aag cag ttt 144
 Lys Arg Arg His Pro Lys Lys Leu Thr Pro Leu Ala Tyr Lys Gln Phe
 35 40 45

att ccc aac gta gcc gag aag acc cta ggg gcc agc ggc aga tat gaa 192
 Ile Pro Asn Val Ala Glu Lys Thr Leu Gly Ala Ser Gly Arg Tyr Glu
 50 55 60

ggg aag atc aca aga aac tcc gaa cga ttt aag gaa ctc acc ccc aat 240
 Gly Lys Ile Thr Arg Asn Ser Glu Arg Phe Lys Glu Leu Thr Pro Asn
 65 70 75 80

tac aac ccc gac atc ata ttt aag gat gag gaa aac acg gga gca gac 288
 Tyr Asn Pro Asp Ile Ile Phe Lys Asp Glu Glu Asn Thr Gly Ala Asp
 85 90 95

cgg	ctg	atg	act	cag	agg	tgc	aaa	gac	aag	tta	aat	gcc	ttg	gcc	atc	336
Arg	Leu	Met	Thr	Gln	Arg	Cys	Lys	Asp	Lys	Leu	Asn	Ala	Leu	Ala	Ile	
			100					105					110			
tct	gtg	atg	aac	cag	tgg	cct	gga	gtg	agg	ctg	cga	gtg	acc	gag	ggc	384
Ser	Val	Met	Asn	Gln	Trp	Pro	Gly	Val	Arg	Leu	Arg	Val	Thr	Glu	Gly	
			115				120					125				
tgg	gat	gag	gac	ggc	cat	cat	tca	gag	gag	tct	cta	cac	tat	gag	ggc	432
Trp	Asp	Glu	Asp	Gly	His	His	Ser	Glu	Glu	Ser	Leu	His	Tyr	Glu	Gly	
	130						135				140					
cga	gca	gtg	gac	atc	acc	acg	tcc	gac	cgg	gac	cgc	agc	aag	tac	ggc	480
Arg	Ala	Val	Asp	Ile	Thr	Thr	Ser	Asp	Arg	Asp	Arg	Ser	Lys	Tyr	Gly	
145					150					155					160	
atg	ctg	gct	cgc	ctg	gct	gtg	gaa	gca	ggc	ttc	gac	tgg	gtc	tac	tat	528
Met	Leu	Ala	Arg	Leu	Ala	Val	Glu	Ala	Gly	Phe	Asp	Trp	Val	Tyr	Tyr	
				165					170					175		
gaa	tcc	aaa	gct	cac	atc	cac	tgt	tct	gtg	aaa	gca	gag	aac	tcc	gtg	576
Glu	Ser	Lys	Ala	His	Ile	His	Cys	Ser	Val	Lys	Ala	Glu	Asn	Ser	Val	
			180					185					190			
gcg	gcc	aaa	tcc	ggc	ggc	tgt	ttc	ccg	gga	tcc	gcc	acc	gtg	cac	ctg	624
Ala	Ala	Lys	Ser	Gly	Gly	Cys	Phe	Pro	Gly	Ser	Ala	Thr	Val	His	Leu	
		195					200					205				
gag	cag	ggc	ggc	acc	aag	ctg	gtg	aag	gac	tta	cgt	ccc	gga	gac	cgc	672
Glu	Gln	Gly	Gly	Thr	Lys	Leu	Val	Lys	Asp	Leu	Arg	Pro	Gly	Asp	Arg	
	210					215					220					
gtg	ctg	gcg	gct	gac	gac	cag	ggc	cgg	ctg	ctg	tac	agc	gac	ttc	ctc	720
Val	Leu	Ala	Ala	Asp	Asp	Gln	Gly	Arg	Leu	Leu	Tyr	Ser	Asp	Phe	Leu	
225					230					235					240	
acc	ttc	ctg	gac	cgc	gac	gaa	ggc	gcc	aag	aag	gtc	ttc	tac	gtg	atc	768
Thr	Phe	Leu	Asp	Arg	Asp	Glu	Gly	Ala	Lys	Lys	Val	Phe	Tyr	Val	Ile	
				245					250					255		
gag	acg	ctg	gag	ccg	cgc	gag	cgc	ctg	ctg	ctc	acc	gcc	gcg	cac	ctg	816
Glu	Thr	Leu	Glu	Pro	Arg	Glu	Arg	Leu	Leu	Leu	Thr	Ala	Ala	His	Leu	
			260					265					270			
ctc	ttc	gtg	gcg	ccg	cac	aac	gac	tgc	ggg	ccc	acg	ccc	ggg	cca	agc	864
Leu	Phe	Val	Ala	Pro	His	Asn	Asp	Ser	Gly	Pro	Thr	Pro	Gly	Pro	Ser	
		275					280					285				
gcg	ctc	ttt	gcc	agc	cgc	gtg	cgc	ccc	ggg	cag	cgc	gtg	tac	gtg	gtg	912
Ala	Leu	Phe	Ala	Ser	Arg	Val	Arg	Pro	Gly	Gln	Arg	Val	Tyr	Val	Val	
	290					295				300						
gct	gaa	cgc	ggc	ggg	gac	cgc	cgg	ctg	ctg	ccc	gcc	gcg	gtg	cac	agc	960
Ala	Glu	Arg	Gly	Gly	Asp	Arg	Arg	Leu	Leu	Pro	Ala	Ala	Val	His	Ser	
305					310					315					320	

gtg acg ctg cga gag gag gag gcg ggc gcg tac gcg ccg ctc acg gcg 1008
Val Thr Leu Arg Glu Glu Glu Ala Gly Ala Tyr Ala Pro Leu Thr Ala
325 330 335

cac ggc acc att ctc atc aac cgg gtg ctc gcc tcg tgc tac gct gtc 1056
His Gly Thr Ile Leu Ile Asn Arg Val Leu Ala Ser Cys Tyr Ala Val
340 345 350

atc gag gag cac agc tgg gca cac cgg gcc ttc gcg cct ttc cgc ctg 1104
Ile Glu Glu His Ser Trp Ala His Arg Ala Phe Ala Pro Phe Arg Leu
355 360 365

gcg cac gcg ctg ctg gcc gcg ctg gca ccc gcc cgc acg gac ggc ggg 1152
Ala His Ala Leu Leu Ala Ala Leu Ala Pro Ala Arg Thr Asp Gly Gly
370 375 380

ggc ggg ggc agc atc cct gca gcg caa tct gca acg gaa gcg agg ggc 1200
Gly Gly Gly Ser Ile Pro Ala Ala Gln Ser Ala Thr Glu Ala Arg Gly
385 390 395 400

gcg gag ccg act gcg ggc atc cac tgg tac tcg cag ctg ctc tac cac 1248
Ala Glu Pro Thr Ala Gly Ile His Trp Tyr Ser Gln Leu Leu Tyr His
405 410 415

att ggc acc tgg ctg ttg gac agc gag acc atg cat ccc ttg gga atg 1296
Ile Gly Thr Trp Leu Leu Asp Ser Glu Thr Met His Pro Leu Gly Met
420 425 430

gcg gtc aag tcc agc tg 1313
Ala Val Lys Ser Ser
435

<210> 5
<211> 1256
<212> DNA
<213> Brachydanio rerio

<220>
<221> CDS
<222> (1)..(1254)

<400> 5
atg cgg ctt ttg acg aga gtg ctg ctg gtg tct ctt ctc act ctg tcc 48
Met Arg Leu Leu Thr Arg Val Leu Leu Val Ser Leu Leu Thr Leu Ser
1 5 10 15

ttg gtg gtg tcc gga ctg gcc tgc ggt cct ggc aga ggc tac ggc aga 96
Leu Val Val Ser Gly Leu Ala Cys Gly Pro Gly Arg Gly Tyr Gly Arg
20 25 30

aga aga cat ccg aag aag ctg aca cct ctc gcc tac aag cag ttc ata 144
Arg Arg His Pro Lys Lys Leu Thr Pro Leu Ala Tyr Lys Gln Phe Ile
35 40 45

cct aat gtc gcg gag aag acc tta ggg gcc agc ggc aga tac gag ggc 192
Pro Asn Val Ala Glu Lys Thr Leu Gly Ala Ser Gly Arg Tyr Glu Gly
50 55 60

NOV 24 2000

10

aag ata acg cgc aat tcg gag aga ttt aaa gaa ctt act cca aat tac	240
Lys Ile Thr Arg Asn Ser Glu Arg Phe Lys Glu Leu Thr Pro Asn Tyr	
65 70 75 80	
aat ccc gac att atc ttt aag gat gag gag aac acg gga gcg gac agg	288
Asn Pro Asp Ile Ile Phe Lys Asp Glu Glu Asn Thr Gly Ala Asp Arg	
85 90 95	
ctc atg aca cag aga tgc aaa gac aag ctg aac tcg ctg gcc atc tct	336
Leu Met Thr Gln Arg Cys Lys Asp Lys Leu Asn Ser Leu Ala Ile Ser	
100 105 110	
gta atg aac cac tgg cca ggg gtt aag ctg cgt gtg aca gag ggc tgg	384
Val Met Asn His Trp Pro Gly Val Lys Leu Arg Val Thr Glu Gly Trp	
115 120 125	
gat gag gac ggt cac cat ttt gaa gaa tca ctc cac tac gag gga aga	432
Asp Glu Asp Gly His His Phe Glu Glu Ser Leu His Tyr Glu Gly Arg	
130 135 140	
gct gtt gat att acc acc tct gac cga gac aag agc aaa tac ggg aca	480
Ala Val Asp Ile Thr Thr Ser Asp Arg Asp Lys Ser Lys Tyr Gly Thr	
145 150 155 160	
ctg tct cgc cta gct gtg gag gct gga ttt gac tgg gtc tat tac gag	528
Leu Ser Arg Leu Ala Val Glu Ala Gly Phe Asp Trp Val Tyr Tyr Glu	
165 170 175	
tcc aaa gcc cac att cat tgc tct gtc aaa gca gaa aat tcg gtt gct	576
Ser Lys Ala His Ile His Cys Ser Val Lys Ala Glu Asn Ser Val Ala	
180 185 190	
gcg aaa tct ggg ggc tgt ttc cca ggt tcg gct ctg gtc tcg ctc cag	624
Ala Lys Ser Gly Gly Cys Phe Pro Gly Ser Ala Leu Val Ser Leu Gln	
195 200 205	
gac gga gga cag aag gcc gtg aag gac ctg aac ccc gga gac aag gtg	672
Asp Gly Gly Gln Lys Ala Val Lys Asp Leu Asn Pro Gly Asp Lys Val	
210 215 220	
ctg gcg gca gac agc gcg gga aac ctg gtg ttc agc gac ttc atc atg	720
Leu Ala Ala Asp Ser Ala Gly Asn Leu Val Phe Ser Asp Phe Ile Met	
225 230 235 240	
ttc aca gac cga gac tcc acg acg cga cgt gtg ttt tac gtc ata gaa	768
Phe Thr Asp Arg Asp Ser Thr Thr Arg Arg Val Phe Tyr Val Ile Glu	
245 250 255	
acg caa gaa ccc gtt gaa aag atc acc ctc acc gcc gct cac ctc ctt	816
Thr Gln Glu Pro Val Glu Lys Ile Thr Leu Thr Ala Ala His Leu Leu	
260 265 270	
ttt gtc ctc gac aac tca acg gaa gat ctc cac acc atg acc gcc gcg	864
Phe Val Leu Asp Asn Ser Thr Glu Asp Leu His Thr Met Thr Ala Ala	
275 280 285	

TECH CENTER 1600/2800

tat gcc agc agt gtc aga gcc gga caa aag gtg atg gtt gtt gat gat	912
Tyr Ala Ser Ser Val Arg Ala Gly Gln Lys Val Met Val Val Asp Asp	
290 295 300	
agc ggt cag ctt aaa tct gtc atc gtg cag cgg ata tac acg gag gag	960
Ser Gly Gln Leu Lys Ser Val Ile Val Gln Arg Ile Tyr Thr Glu Glu	
305 310 315 320	
cag cgg ggc tcg ttc gca cca gtg act gca cat ggg acc att gtg gtc	1008
Gln Arg Gly Ser Phe Ala Pro Val Thr Ala His Gly Thr Ile Val Val	
325 330 335	
gac aga ata ctg gcg tcc tgt tac gcc gta ata gag gac cag ggg ctt	1056
Asp Arg Ile Leu Ala Ser Cys Tyr Ala Val Ile Glu Asp Gln Gly Leu	
340 345 350	
gcg cat ttg gcc ttc gcg ccc gcc agg ctc tat tat tac gtg tca tca	1104
Ala His Leu Ala Phe Ala Pro Ala Arg Leu Tyr Tyr Tyr Val Ser Ser	
355 360 365	
ttc ctg tcc ccc aaa act cca gca gtc ggt cca atg cga ctt tac aac	1152
Phe Leu Ser Pro Lys Thr Pro Ala Val Gly Pro Met Arg Leu Tyr Asn	
370 375 380	
agg agg ggg tcc act ggt act cca ggc tcc tgt cat caa atg gga acg	1200
Arg Arg Gly Ser Thr Gly Thr Pro Gly Ser Cys His Gln Met Gly Thr	
385 390 395 400	
tgg ctt ttg gac agc aac atg ctt cat cct ttg ggg atg tca gta aac	1248
Trp Leu Leu Asp Ser Asn Met Leu His Pro Leu Gly Met Ser Val Asn	
405 410 415	
tca agc tg	1256
Ser Ser	

<210> 6
 <211> 1425
 <212> DNA
 <213> Homo sapien

<220>
 <221> CDS
 <222> (1)..(1425)

<220>
 <221> MOD_RES
 <222> (1397)..(1389)
 <223> a, t, c, g, other or unknown

<400> 6	
atg ctg ctg ctg gcg aga tgt ctg ctg cta gtc ctc gtc tcc tcg ctg	48
Met Leu Leu Leu Ala Arg Cys Leu Leu Leu Val Leu Val Ser Ser Leu	
1 5 10 15	
ctg gta tgc tcg gga ctg gcg tgc gga ccg ggc agg ggg ttc ggg aag	96
Leu Val Cys Ser Gly Leu Ala Cys Gly Pro Gly Arg Gly Phe Gly Lys	
20 25 30	

agg	agg	cac	ccc	aaa	aag	ctg	acc	cct	tta	gcc	tac	aag	cag	ttt	atc	144
Arg	Arg	His	Pro	Lys	Lys	Leu	Thr	Pro	Leu	Ala	Tyr	Lys	Gln	Phe	Ile	
		35					40					45				
ccc	aat	gtg	gcc	gag	aag	acc	cta	ggc	gcc	agc	gga	agg	tat	gaa	ggg	192
Pro	Asn	Val	Ala	Glu	Lys	Thr	Leu	Gly	Ala	Ser	Gly	Arg	Tyr	Glu	Gly	
	50					55					60					
aag	atc	tcc	aga	aac	tcc	gag	cga	ttt	aag	gaa	ctc	acc	ccc	aat	tac	240
Lys	Ile	Ser	Arg	Asn	Ser	Glu	Arg	Phe	Lys	Glu	Leu	Thr	Pro	Asn	Tyr	
	65				70					75					80	
aac	ccc	gac	atc	ata	ttt	aag	gat	gaa	gaa	aac	acc	gga	gcg	gac	agg	288
Asn	Pro	Asp	Ile	Ile	Phe	Lys	Asp	Glu	Glu	Asn	Thr	Gly	Ala	Asp	Arg	
				85					90					95		
ctg	atg	act	cag	agg	tgt	aag	gac	aag	ttg	aac	gct	ttg	gcc	atc	tcg	336
Leu	Met	Thr	Gln	Arg	Cys	Lys	Asp	Lys	Leu	Asn	Ala	Leu	Ala	Ile	Ser	
			100					105					110			
gtg	atg	aac	cag	tgg	cca	gga	gtg	aaa	ctg	cgg	gtg	acc	gag	ggc	tgg	384
Val	Met	Asn	Gln	Trp	Pro	Gly	Val	Lys	Leu	Arg	Val	Thr	Glu	Gly	Trp	
		115					120					125				
gac	gaa	gat	ggc	cac	cac	tca	gag	gag	tct	ctg	cac	tac	gag	ggc	cgc	432
Asp	Glu	Asp	Gly	His	His	Ser	Glu	Glu	Ser	Leu	His	Tyr	Glu	Gly	Arg	
	130					135					140					
gca	gtg	gac	atc	acc	acg	tct	gac	cgc	gac	cgc	agc	aag	tac	ggc	atg	480
Ala	Val	Asp	Ile	Thr	Thr	Ser	Asp	Arg	Asp	Arg	Ser	Lys	Tyr	Gly	Met	
	145				150					155					160	
ctg	gcc	cgc	ctg	gcg	gtg	gag	gcc	ggc	ttc	gac	tgg	gtg	tac	tac	gag	528
Leu	Ala	Arg	Leu	Ala	Val	Glu	Ala	Gly	Phe	Asp	Trp	Val	Tyr	Tyr	Glu	
				165					170					175		
tcc	aag	gca	cat	atc	cac	tgc	tcg	gtg	aaa	gca	gag	aac	tcg	gtg	gcg	576
Ser	Lys	Ala	His	Ile	His	Cys	Ser	Val	Lys	Ala	Glu	Asn	Ser	Val	Ala	
			180					185					190			
gcc	aaa	tcg	gga	ggc	tgc	ttc	ccg	ggc	tcg	gcc	acg	gtg	cac	ctg	gag	624
Ala	Lys	Ser	Gly	Gly	Cys	Phe	Pro	Gly	Ser	Ala	Thr	Val	His	Leu	Glu	
		195					200					205				
cag	ggc	ggc	acc	aag	ctg	gtg	aag	gac	ctg	agc	ccc	ggg	gac	cgc	gtg	672
Gln	Gly	Gly	Thr	Lys	Leu	Val	Lys	Asp	Leu	Ser	Pro	Gly	Asp	Arg	Val	
	210					215					220					
ctg	gcg	gcg	gac	gac	cag	ggc	cgg	ctg	ctc	tac	agc	gac	ttc	ctc	act	720
Leu	Ala	Ala	Asp	Asp	Gln	Gly	Arg	Leu	Leu	Tyr	Ser	Asp	Phe	Leu	Thr	
	225				230					235					240	
ttc	ctg	gac	cgc	gac	gac	ggc	gcc	aag	aag	gtc	ttc	tac	gtg	atc	gag	768
Phe	Leu	Asp	Arg	Asp	Asp	Gly	Ala	Lys	Lys	Val	Phe	Tyr	Val	Ile	Glu	
				245					250					255		

acg cgg gag ccg cgc gag cgc ctg ctg ctc acc gcc gcg cac ctg ctc	816
Thr Arg Glu Pro Arg Glu Arg Leu Leu Leu Thr Ala Ala His Leu Leu	
260 265 270	
ttt gtg gcg ccg cac aac gac tcg gcc acc ggg gag ccc gag gcg tcc	864
Phe Val Ala Pro His Asn Asp Ser Ala Thr Gly Glu Pro Glu Ala Ser	
275 280 285	
tcg ggc tcg ggg ccg cct tcc ggg ggc gca ctg ggg cct cgg gcg ctg	912
Ser Gly Ser Gly Pro Pro Ser Gly Gly Ala Leu Gly Pro Arg Ala Leu	
290 295 300	
ttc gcc agc cgc gtg cgc ccg ggc cag cgc gtg tac gtg gtg gcc gag	960
Phe Ala Ser Arg Val Arg Pro Gly Gln Arg Val Tyr Val Val Ala Glu	
305 310 315 320	
cgt gac ggg gac cgc cgg ctc ctg ccc gcc gct gtg cac agc gtg acc	1008
Arg Asp Gly Asp Arg Arg Leu Leu Pro Ala Ala Val His Ser Val Thr	
325 330 335	
cta agc gag gag gcc gcg ggc gcc tac gcg ccg ctc acg gcc cag ggc	1056
Leu Ser Glu Glu Ala Ala Gly Ala Tyr Ala Pro Leu Thr Ala Gln Gly	
340 345 350	
acc att ctc atc aac cgg gtg ctg gcc tcg tgc tac gcg gtc atc gag	1104
Thr Ile Leu Ile Asn Arg Val Leu Ala Ser Cys Tyr Ala Val Ile Glu	
355 360 365	
gag cac agc tgg gcg cac cgg gcc ttc gcg ccc ttc cgc ctg gcg cac	1152
Glu His Ser Trp Ala His Arg Ala Phe Ala Pro Phe Arg Leu Ala His	
370 375 380	
gcg ctc ctg gct gca ctg gcg ccc gcg cgc acg gac cgc ggc ggg gac	1200
Ala Leu Leu Ala Ala Leu Ala Pro Ala Arg Thr Asp Arg Gly Gly Asp	
385 390 395 400	
agc ggc ggc ggg gac cgc ggg ggc ggc ggc ggc aga gta gcc cta acc	1248
Ser Gly Gly Gly Asp Arg Gly Gly Gly Gly Gly Arg Val Ala Leu Thr	
405 410 415	
gct cca ggt gct gcc gac gct ccg ggt gcg ggg gcc acc gcg ggc atc	1296
Ala Pro Gly Ala Ala Asp Ala Pro Gly Ala Gly Ala Thr Ala Gly Ile	
420 425 430	
cac tgg tac tcg cag ctg ctc tac caa ata ggc acc tgg ctc ctg gac	1344
His Trp Tyr Ser Gln Leu Leu Tyr Gln Ile Gly Thr Trp Leu Leu Asp	
435 440 445	
agc gag gcc ctg cac ccg ctg ggc atg gcg gtc aag tcc agc nnn agc	1392
Ser Glu Ala Leu His Pro Leu Gly Met Ala Val Lys Ser Ser Xaa Ser	
450 455 460	
cgg ggg gcc ggg gga ggg gcg cgg gag ggg gcc	1425
Arg Gly Ala Gly Gly Gly Ala Arg Glu Gly Ala	
465 470 475	

<210> 7

<211> 1622

<212> DNA

<213> Homo sapien

<220>

<221> CDS

<222> (51)..(1283)

<400> 7

```

catcagccca ccaggagacc tcgcccgcgc ctcccccgcc ctcccccgcc atg tct      56
                                     Met Ser
                                     1

ccc gcc cgg ctc cgg ccc cga ctg cac ttc tgc ctg gtc ctg ttg ctg      104
Pro Ala Arg Leu Arg Pro Arg Leu His Phe Cys Leu Val Leu Leu Leu
          5                      10                      15

ctg ctg gtg gtg ccc gcg gca tgg ggc tgc ggg ccg ggt cgg gtg gtg      152
Leu Leu Val Val Pro Ala Ala Trp Gly Cys Gly Pro Gly Arg Val Val
      20                      25                      30

ggc agc cgc cgg cga ccg cca cgc aaa ctc gtg ccg ctc gcc tac aag      200
Gly Ser Arg Arg Arg Pro Pro Arg Lys Leu Val Pro Leu Ala Tyr Lys
      35                      40                      45                      50

cag ttc agc ccc aat gtg ccc gag aag acc ctg ggc gcc agc gga cgc      248
Gln Phe Ser Pro Asn Val Pro Glu Lys Thr Leu Gly Ala Ser Gly Arg
          55                      60                      65

tat gaa ggc aag atc gct cgc agc tcc gag cgc ttc aag gag ctc acc      296
Tyr Glu Gly Lys Ile Ala Arg Ser Ser Glu Arg Phe Lys Glu Leu Thr
          70                      75                      80

ccc aat tac aat cca gac atc atc ttc aag gac gag gag aac aca ggc      344
Pro Asn Tyr Asn Pro Asp Ile Ile Phe Lys Asp Glu Glu Asn Thr Gly
          85                      90                      95

gcc gac cgc ctc atg acc cag cgc tgc aag gac cgc ctg aac tcg ctg      392
Ala Asp Arg Leu Met Thr Gln Arg Cys Lys Asp Arg Leu Asn Ser Leu
      100                      105                      110

gct atc tcg gtg atg aac cag tgg ccc ggt gtg aag ctg cgg gtg acc      440
Ala Ile Ser Val Met Asn Gln Trp Pro Gly Val Lys Leu Arg Val Thr
      115                      120                      125                      130

gag ggc tgg gac gag gac ggc cac cac tca gag gag tcc ctg cat tat      488
Glu Gly Trp Asp Glu Asp Gly His His Ser Glu Glu Ser Leu His Tyr
          135                      140                      145

gag ggc cgc gcg gtg gac atc acc aca tca gac cgc gac cgc aat aag      536
Glu Gly Arg Ala Val Asp Ile Thr Thr Ser Asp Arg Asp Arg Asn Lys
          150                      155                      160

tat gga ctg ctg gcg cgc ttg gca gtg gag gcc ggc ttt gac tgg gtg      584
Tyr Gly Leu Leu Ala Arg Leu Ala Val Glu Ala Gly Phe Asp Trp Val
          165                      170                      175

```

tat	tac	gag	tca	aag	gcc	cac	gtg	cat	tgc	tcc	gtc	aag	tcc	gag	cac	632
Tyr	Tyr	Glu	Ser	Lys	Ala	His	Val	His	Cys	Ser	Val	Lys	Ser	Glu	His	
180						185					190					
tcg	gcc	gca	gcc	aag	acg	ggc	ggc	tgc	ttc	cct	gcc	gga	gcc	cag	gta	680
Ser	Ala	Ala	Ala	Lys	Thr	Gly	Gly	Cys	Phe	Pro	Ala	Gly	Ala	Gln	Val	
195					200					205					210	
cgc	ctg	gag	agt	ggg	gcg	cgt	gtg	gcc	ttg	tca	gcc	gtg	agg	ccg	gga	728
Arg	Leu	Glu	Ser	Gly	Ala	Arg	Val	Ala	Leu	Ser	Ala	Val	Arg	Pro	Gly	
				215					220					225		
gac	cgt	gtg	ctg	gcc	atg	ggg	gag	gat	ggg	agc	ccc	acc	ttc	agc	gat	776
Asp	Arg	Val	Leu	Ala	Met	Gly	Glu	Asp	Gly	Ser	Pro	Thr	Phe	Ser	Asp	
			230					235					240			
gtg	ctc	att	ttc	ctg	gac	cgc	gag	ccc	cac	agg	ctg	aga	gcc	ttc	cag	824
Val	Leu	Ile	Phe	Leu	Asp	Arg	Glu	Pro	His	Arg	Leu	Arg	Ala	Phe	Gln	
		245					250					255				
gtc	atc	gag	act	cag	gac	ccc	cca	cgc	cgc	ctg	gca	ctc	aca	ccc	gct	872
Val	Ile	Glu	Thr	Gln	Asp	Pro	Pro	Arg	Arg	Leu	Ala	Leu	Thr	Pro	Ala	
	260					265					270					
cac	ctg	ctc	ttt	acg	gct	gac	aat	cac	acg	gag	ccg	gca	gcc	cgc	ttc	920
His	Leu	Leu	Phe	Thr	Ala	Asp	Asn	His	Thr	Glu	Pro	Ala	Ala	Arg	Phe	
275					280					285					290	
cgg	gcc	aca	ttt	gcc	agc	cac	gtg	cag	cct	ggc	cag	tac	gtg	ctg	gtg	968
Arg	Ala	Thr	Phe	Ala	Ser	His	Val	Gln	Pro	Gly	Gln	Tyr	Val	Leu	Val	
				295					300					305		
gct	ggg	gtg	cca	ggc	ctg	cag	cct	gcc	cgc	gtg	gca	gct	gtc	tct	aca	1016
Ala	Gly	Val	Pro	Gly	Leu	Gln	Pro	Ala	Arg	Val	Ala	Ala	Val	Ser	Thr	
			310					315					320			
cac	gtg	gcc	ctc	ggg	gcc	tac	gcc	ccg	ctc	aca	aag	cat	ggg	aca	ctg	1064
His	Val	Ala	Leu	Gly	Ala	Tyr	Ala	Pro	Leu	Thr	Lys	His	Gly	Thr	Leu	
		325					330					335				
gtg	gtg	gag	gat	gtg	gtg	gca	tcc	tgc	ttc	gcg	gcc	gtg	gct	gac	cac	1112
Val	Val	Glu	Asp	Val	Val	Ala	Ser	Cys	Phe	Ala	Ala	Val	Ala	Asp	His	
	340					345					350					
cac	ctg	gct	cag	ttg	gcc	ttc	tgg	ccc	ctg	aga	ctc	ttt	cac	agc	ttg	1160
His	Leu	Ala	Gln	Leu	Ala	Phe	Trp	Pro	Leu	Arg	Leu	Phe	His	Ser	Leu	
355					360					365					370	
gca	tgg	ggc	agc	tgg	acc	ccg	ggg	gag	ggg	gtg	cat	tgg	tac	ccc	cag	1208
Ala	Trp	Gly	Ser	Trp	Thr	Pro	Gly	Glu	Gly	Val	His	Trp	Tyr	Pro	Gln	
				375					380					385		
ctg	ctc	tac	cgc	ctg	ggg	cgt	ctc	ctg	cta	gaa	gag	ggc	agc	ttc	cac	1256
Leu	Leu	Tyr	Arg	Leu	Gly	Arg	Leu	Leu	Leu	Glu	Glu	Gly	Ser	Phe	His	
			390					395					400			

NOV 24 2000

16

cca ctg ggc atg tcc ggg gca ggg agc tgaaaggact ccaccgctgc
 Pro Leu Gly Met Ser Gly Ala Gly Ser
 405 410

1303 TECH CENTER 1600/2000

cctcctggaa ctgctgtact ggggtccagaa gcctctcagc caggagggag ctggccctgg 1363
 aagggacctg agctggggga cactggctcc tgccatctcc tctgccatga agatacacca 1423
 ttgagacttg actgggcaac accagcgtcc cccaccgcg tctgtggtgta gtcatagagc 1483
 tgcaagctga gctggcgagg ggatggttgt tgaccctct ctctagaga ccttgaggct 1543
 ggcacggcga ctcccaactc agcctgctct cactacgagt ttccatactc tgccctcccc 1603
 attgggaggg cccattccc 1622

<210> 8
 <211> 1190
 <212> DNA
 <213> Homo sapien

<220>
 <221> CDS
 <222> (1)..(1188)

<400> 8
 atg gct ctc ctg acc aat cta ctg ccc ttg tgc tgc ttg gca ctt ctg 48
 Met Ala Leu Leu Thr Asn Leu Leu Pro Leu Cys Cys Leu Ala Leu Leu
 1 5 10 15
 gcg ctg cca gcc cag agc tgc ggg ccg ggc cgg ggg ccg gtt ggc cgg 96
 Ala Leu Pro Ala Gln Ser Cys Gly Pro Gly Arg Gly Pro Val Gly Arg
 20 25 30
 cgc cgc tat gcg cgc aag cag ctc gtg ccg cta ctc tac aag caa ttt 144
 Arg Arg Tyr Ala Arg Lys Gln Leu Val Pro Leu Leu Tyr Lys Gln Phe
 35 40 45
 gtg ccc ggc gtg cca gag cgg acc ctg ggc gcc agt ggg cca gcg gag 192
 Val Pro Gly Val Pro Glu Arg Thr Leu Gly Ala Ser Gly Pro Ala Glu
 50 55 60
 ggg agg gtg gca agg ggc tcc gag cgc ttc cgg gac ctc gtg ccc aac 240
 Gly Arg Val Ala Arg Gly Ser Glu Arg Phe Arg Asp Leu Val Pro Asn
 65 70 75 80
 tac aac ccc gac atc atc ttc aag gat gag gag aac agt gga gcc gac 288
 Tyr Asn Pro Asp Ile Ile Phe Lys Asp Glu Glu Asn Ser Gly Ala Asp
 85 90 95
 cgc ctg atg acc gag cgt tgc aag gag agg gtg aac gct ttg gcc att 336
 Arg Leu Met Thr Glu Arg Cys Lys Glu Arg Val Asn Ala Leu Ala Ile
 100 105 110
 gcc gtg atg aac atg tgg ccc gga gtg cgc cta cga gtg act gag ggc 384
 Ala Val Met Asn Met Trp Pro Gly Val Arg Leu Arg Val Thr Glu Gly
 115 120 125

tgg gac gag gac ggc cac cac gct cag gat tca ctc cac tac gaa ggc	432
Trp Asp Glu Asp Gly His His Ala Gln Asp Ser Leu His Tyr Glu Gly	
130 135 140	
cgt gct ttg gac atc act acg tct gac cgc gac cgc aac aag tat ggg	480
Arg Ala Leu Asp Ile Thr Thr Ser Asp Arg Asp Arg Asn Lys Tyr Gly	
145 150 155 160	
ttg ctg gcg cgc ctc gca gtg gaa gcc ggc ttc gac tgg gtc tac tac	528
Leu Leu Ala Arg Leu Ala Val Glu Ala Gly Phe Asp Trp Val Tyr Tyr	
165 170 175	
gag tcc cgc aac cac gtc cac gtg tcg gtc aaa gct gat aac tca ctg	576
Glu Ser Arg Asn His Val His Val Ser Val Lys Ala Asp Asn Ser Leu	
180 185 190	
gcg gtc cgg gcg ggc ggc tgc ttt ccg gga aat gca act gtg cgc ctg	624
Ala Val Arg Ala Gly Gly Cys Phe Pro Gly Asn Ala Thr Val Arg Leu	
195 200 205	
tgg agc ggc gag cgg aaa ggg ctg cgg gaa ctg cac cgc gga gac tgg	672
Trp Ser Gly Glu Arg Lys Gly Leu Arg Glu Leu His Arg Gly Asp Trp	
210 215 220	
gtt ttg gcg gcc gat gcg tca ggc cgg gtg gtg ccc acg ccg gtg ctg	720
Val Leu Ala Ala Asp Ala Ser Gly Arg Val Val Pro Thr Pro Val Leu	
225 230 235 240	
ctc ttc ctg gac cgg gac ttg cag cgc cgg gct tca ttt gtg gct gtg	768
Leu Phe Leu Asp Arg Asp Leu Gln Arg Arg Ala Ser Phe Val Ala Val	
245 250 255	
gag acc gag tgg cct cca cgc aaa ctg ttg ctc acg ccc tgg cac ctg	816
Glu Thr Glu Trp Pro Pro Arg Lys Leu Leu Leu Thr Pro Trp His Leu	
260 265 270	
gtg ttt gcc gct cga ggg ccg gcg ccc gcg cca ggc gac ttt gca ccg	864
Val Phe Ala Ala Arg Gly Pro Ala Pro Ala Pro Gly Asp Phe Ala Pro	
275 280 285	
gtg ttc gcg cgc cgg cta cgc gct ggg gac tcg gtg ctg gcg ccc ggc	912
Val Phe Ala Arg Arg Leu Arg Ala Gly Asp Ser Val Leu Ala Pro Gly	
290 295 300	
ggg gat gcg ctt cgg cca gcg cgc gtg gcc cgt gtg gcg cgg gag gaa	960
Gly Asp Ala Leu Arg Pro Ala Arg Val Ala Arg Val Ala Arg Glu Glu	
305 310 315 320	
gcc gtg ggc gtg ttc gcg ccg ctc acc gcg cac ggg acg ctg ctg gtg	1008
Ala Val Gly Val Phe Ala Pro Leu Thr Ala His Gly Thr Leu Leu Val	
325 330 335	
aac gat gtc ctg gcc tct tgc tac gcg gtt ctg gag agt cac cag tgg	1056
Asn Asp Val Leu Ala Ser Cys Tyr Ala Val Leu Glu Ser His Gln Trp	
340 345 350	

```

gcg cac cgc gct ttt gcc ccc ttg aga ctg ctg cac gcg cta ggg gcg 1104
Ala His Arg Ala Phe Ala Pro Leu Arg Leu Leu His Ala Leu Gly Ala
      355                      360                      365

ctg ctc ccc ggc ggg gcc gtc cag ccg act ggc atg cat tgg tac tct 1152
Leu Leu Pro Gly Gly Ala Val Gln Pro Thr Gly Met His Trp Tyr Ser
      370                      375                      380

cgg ctc ctc tac cgc tta gcg gag gag cta ctg ggc tg 1190
Arg Leu Leu Tyr Arg Leu Ala Glu Glu Leu Leu Gly
385                      390                      395

<210> 9
<211> 1251
<212> DNA
<213> Brachydanio rerio

<220>
<221> CDS
<222> (1)..(1248)

<400> 9
atg gac gta agg ctg cat ctg aag caa ttt gct tta ctg tgt ttt atc 48
Met Asp Val Arg Leu His Leu Lys Gln Phe Ala Leu Leu Cys Phe Ile
      1                      5                      10                      15

agc ttg ctt ctg acg cct tgt gga tta gcc tgt ggt cct ggt aga ggt 96
Ser Leu Leu Leu Thr Pro Cys Gly Leu Ala Cys Gly Pro Gly Arg Gly
      20                      25                      30

tat gga aaa cga aga cac cca aag aaa tta acc ccg ttg gct tac aag 144
Tyr Gly Lys Arg Arg His Pro Lys Lys Leu Thr Pro Leu Ala Tyr Lys
      35                      40                      45

caa ttc atc ccc aac gtt gct gag aaa acg ctt gga gcc agc ggc aaa 192
Gln Phe Ile Pro Asn Val Ala Glu Lys Thr Leu Gly Ala Ser Gly Lys
      50                      55                      60

tac gaa ggc aaa atc aca agg aat tca gag aga ttt aaa gag ctg att 240
Tyr Glu Gly Lys Ile Thr Arg Asn Ser Glu Arg Phe Lys Glu Leu Ile
      65                      70                      75                      80

ccg aat tat aat ccc gat atc atc ttt aag gac gag gaa aac aca aac 288
Pro Asn Tyr Asn Pro Asp Ile Ile Phe Lys Asp Glu Glu Asn Thr Asn
      85                      90                      95

gct gac agg ctg atg acc aag cgc tgt aag gac aag tta aat tcg ttg 336
Ala Asp Arg Leu Met Thr Lys Arg Cys Lys Asp Lys Leu Asn Ser Leu
      100                      105                      110

gcc ata tcc gtc atg aac cac tgg ccc ggc gtg aaa ctg cgc gtc act 384
Ala Ile Ser Val Met Asn His Trp Pro Gly Val Lys Leu Arg Val Thr
      115                      120                      125

gaa ggc tgg gat gag gat ggt cac cat tta gaa gaa tct ttg cac tat 432
Glu Gly Trp Asp Glu Asp Gly His His Leu Glu Glu Ser Leu His Tyr
      130                      135                      140

```

gag gga cgg gca gtg gac atc act acc tca gac agg gat aaa agc aag Glu Gly Arg Ala Val Asp Ile Thr Thr Ser Asp Arg Asp Lys Ser Lys 145 150 155 160	480
tat ggg atg cta tcc agg ctt gca gtg gag gca gga ttc gac tgg gtc Tyr Gly Met Leu Ser Arg Leu Ala Val Glu Ala Gly Phe Asp Trp Val 165 170 175	528
tat tat gaa tct aaa gcc cac ata cac tgc tct gtc aaa gca gaa aat Tyr Tyr Glu Ser Lys Ala His Ile His Cys Ser Val Lys Ala Glu Asn 180 185 190	576
tca gtg gct gct aaa tca gga gga tgt ttt cct ggg tct ggg acg gtg Ser Val Ala Ala Lys Ser Gly Gly Cys Phe Pro Gly Ser Gly Thr Val 195 200 205	624
aca ctt ggt gat ggg acg agg aaa ccc atc aaa gat ctt aaa gtg ggc Thr Leu Gly Asp Gly Thr Arg Lys Pro Ile Lys Asp Leu Lys Val Gly 210 215 220	672
gac cgg gtt ttg gct gca gac gag aag gga aat gtc tta ata agc gac Asp Arg Val Leu Ala Ala Asp Glu Lys Gly Asn Val Leu Ile Ser Asp 225 230 235 240	720
ttt att atg ttt ata gac cac gat ccg aca acg aga agg caa ttc atc Phe Ile Met Phe Ile Asp His Asp Pro Thr Thr Arg Arg Gln Phe Ile 245 250 255	768
gtc atc gag acg tca gaa cct ttc acc aag ctc acc ctc act gcc gcg Val Ile Glu Thr Ser Glu Pro Phe Thr Lys Leu Thr Leu Thr Ala Ala 260 265 270	816
cac cta gtt ttc gtt gga aac tct tca gca gct tcg ggt ata aca gca His Leu Val Phe Val Gly Asn Ser Ser Ala Ala Ser Gly Ile Thr Ala 275 280 285	864
aca ttt gcc agc aac gtg aag cct gga gat aca gtt tta gtg tgg gaa Thr Phe Ala Ser Asn Val Lys Pro Gly Asp Thr Val Leu Val Trp Glu 290 295 300	912
gac aca tgc gag agc ctc aag agc gtt aca gtg aaa agg att tac act Asp Thr Cys Glu Ser Leu Lys Ser Val Thr Val Lys Arg Ile Tyr Thr 305 310 315 320	960
gag gag cac gag ggc tct ttt gcg cca gtc acc gcg cac gga acc ata Glu Glu His Glu Gly Ser Phe Ala Pro Val Thr Ala His Gly Thr Ile 325 330 335	1008
ata gtg gat cag gtg ttg gca tcg tgc tac gcg gtc att gag aac cac Ile Val Asp Gln Val Leu Ala Ser Cys Tyr Ala Val Ile Glu Asn His 340 345 350	1056
aaa tgg gca cat tgg gct ttt gcg ccg gtc agg ttg tgt cac aag ctg Lys Trp Ala His Trp Ala Phe Ala Pro Val Arg Leu Cys His Lys Leu 355 360 365	1104

atg acg tgg ctt ttt ccg gct cgt gaa tca aac gtc aat ttt cag gag 1152
 Met Thr Trp Leu Phe Pro Ala Arg Glu Ser Asn Val Asn Phe Gln Glu
 370 375 380

gat ggt atc cac tgg tac tca aat atg ctg ttt cac atc ggc tct tgg 1200
 Asp Gly Ile His Trp Tyr Ser Asn Met Leu Phe His Ile Gly Ser Trp
 385 390 395 400

ctg ctg gac aga gac tct ttc cat cca ctc ggg att tta cac tta agt 1248
 Leu Leu Asp Arg Asp Ser Phe His Pro Leu Gly Ile Leu His Leu Ser
 405 410 415

tga 1251

<210> 10
 <211> 425
 <212> PRT
 <213> Gallus sp.

<400> 10
 Met Val Glu Met Leu Leu Leu Thr Arg Ile Leu Leu Val Gly Phe Ile
 1 5 10 15

Cys Ala Leu Leu Val Ser Ser Gly Leu Thr Cys Gly Pro Gly Arg Gly
 20 25 30

Ile Gly Lys Arg Arg His Pro Lys Lys Leu Thr Pro Leu Ala Tyr Lys
 35 40 45

Gln Phe Ile Pro Asn Val Ala Glu Lys Thr Leu Gly Ala Ser Gly Arg
 50 55 60

Tyr Glu Gly Lys Ile Thr Arg Asn Ser Glu Arg Phe Lys Glu Leu Thr
 65 70 75 80

Pro Asn Tyr Asn Pro Asp Ile Ile Phe Lys Asp Glu Glu Asn Thr Gly
 85 90 95

Ala Asp Arg Leu Met Thr Gln Arg Cys Lys Asp Lys Leu Asn Ala Leu
 100 105 110

Ala Ile Ser Val Met Asn Gln Trp Pro Gly Val Lys Leu Arg Val Thr
 115 120 125

Glu Gly Trp Asp Glu Asp Gly His His Ser Glu Glu Ser Leu His Tyr
 130 135 140

Glu Gly Arg Ala Val Asp Ile Thr Thr Ser Asp Arg Asp Arg Ser Lys
 145 150 155 160

Tyr Gly Met Leu Ala Arg Leu Ala Val Glu Ala Gly Phe Asp Trp Val
 165 170 175

Tyr Tyr Glu Ser Lys Ala His Ile His Cys Ser Val Lys Ala Glu Asn
 180 185 190

Ser Val Ala Ala Lys Ser Gly Gly Cys Phe Pro Gly Ser Ala Thr Val
 195 200 205

His Leu Glu His Gly Gly Thr Lys Leu Val Lys Asp Leu Ser Pro Gly
 210 215 220
 Asp Arg Val Leu Ala Ala Asp Ala Asp Gly Arg Leu Leu Tyr Ser Asp
 225 230 235 240
 Phe Leu Thr Phe Leu Asp Arg Met Asp Ser Ser Arg Lys Leu Phe Tyr
 245 250 255
 Val Ile Glu Thr Arg Gln Pro Arg Ala Arg Leu Leu Leu Thr Ala Ala
 260 265 270
 His Leu Leu Phe Val Ala Pro Gln His Asn Gln Ser Glu Ala Thr Gly
 275 280 285
 Ser Thr Ser Gly Gln Ala Leu Phe Ala Ser Asn Val Lys Pro Gly Gln
 290 295 300
 Arg Val Tyr Val Leu Gly Glu Gly Gly Gln Gln Leu Leu Pro Ala Ser
 305 310 315 320
 Val His Ser Val Ser Leu Arg Glu Glu Ala Ser Gly Ala Tyr Ala Pro
 325 330 335
 Leu Thr Ala Gln Gly Thr Ile Leu Ile Asn Arg Val Leu Ala Ser Cys
 340 345 350
 Tyr Ala Val Ile Glu Glu His Ser Trp Ala His Trp Ala Phe Ala Pro
 355 360 365
 Phe Arg Leu Ala Gln Gly Leu Leu Ala Ala Leu Cys Pro Asp Gly Ala
 370 375 380
 Ile Pro Thr Ala Ala Thr Thr Thr Thr Gly Ile His Trp Tyr Ser Arg
 385 390 395 400
 Leu Leu Tyr Arg Ile Gly Ser Trp Val Leu Asp Gly Asp Ala Leu His
 405 410 415
 Pro Leu Gly Met Val Ala Pro Ala Ser
 420 425

<210> 11
 <211> 396
 <212> PRT
 <213> Murine sp.

<400> 11
 Met Ala Leu Pro Ala Ser Leu Leu Pro Leu Cys Cys Leu Ala Leu Leu
 1 5 10 15
 Ala Leu Ser Ala Gln Ser Cys Gly Pro Gly Arg Gly Pro Val Gly Arg
 20 25 30
 Arg Arg Tyr Val Arg Lys Gln Leu Val Pro Leu Leu Tyr Lys Gln Phe
 35 40 45

Val	Pro	Ser	Met	Pro	Glu	Arg	Thr	Leu	Gly	Ala	Ser	Gly	Pro	Ala	Glu	
	50					55					60					
Gly	Arg	Val	Thr	Arg	Gly	Ser	Glu	Arg	Phe	Arg	Asp	Leu	Val	Pro	Asn	
65					70					75					80	
Tyr	Asn	Pro	Asp	Ile	Ile	Phe	Lys	Asp	Glu	Glu	Asn	Ser	Gly	Ala	Asp	
				85					90					95		
Arg	Leu	Met	Thr	Glu	Arg	Cys	Lys	Glu	Arg	Val	Asn	Ala	Leu	Ala	Ile	
			100					105					110			
Ala	Val	Met	Asn	Met	Trp	Pro	Gly	Val	Arg	Leu	Arg	Val	Thr	Glu	Gly	
		115					120					125				
Trp	Asp	Glu	Asp	Gly	His	His	Ala	Gln	Asp	Ser	Leu	His	Tyr	Glu	Gly	
	130					135					140					
Arg	Ala	Leu	Asp	Ile	Thr	Thr	Ser	Asp	Arg	Asp	Arg	Asn	Lys	Tyr	Gly	
145					150					155					160	
Leu	Leu	Ala	Arg	Leu	Ala	Val	Glu	Ala	Gly	Phe	Asp	Trp	Val	Tyr	Tyr	
				165					170					175		
Glu	Ser	Arg	Asn	His	Ile	His	Val	Ser	Val	Lys	Ala	Asp	Asn	Ser	Leu	
			180					185					190			
Ala	Val	Arg	Ala	Gly	Gly	Cys	Phe	Pro	Gly	Asn	Ala	Thr	Val	Arg	Leu	
		195					200					205				
Arg	Ser	Gly	Glu	Arg	Lys	Gly	Leu	Arg	Glu	Leu	His	Arg	Gly	Asp	Trp	
	210					215					220					
Val	Leu	Ala	Ala	Asp	Ala	Ala	Gly	Arg	Val	Val	Pro	Thr	Pro	Val	Leu	
225					230					235					240	
Leu	Phe	Leu	Asp	Arg	Asp	Leu	Gln	Arg	Arg	Ala	Ser	Phe	Val	Ala	Val	
				245					250					255		
Glu	Thr	Glu	Arg	Pro	Pro	Arg	Lys	Leu	Leu	Leu	Thr	Pro	Trp	His	Leu	
			260					265					270			
Val	Phe	Ala	Ala	Arg	Gly	Pro	Ala	Pro	Ala	Pro	Gly	Asp	Phe	Ala	Pro	
	275						280					285				
Val	Phe	Ala	Arg	Arg	Leu	Arg	Ala	Gly	Asp	Ser	Val	Leu	Ala	Pro	Gly	
	290					295					300					
Gly	Asp	Ala	Leu	Gln	Pro	Ala	Arg	Val	Ala	Arg	Val	Ala	Arg	Glu	Glu	
305					310					315				320		
Ala	Val	Gly	Val	Phe	Ala	Pro	Leu	Thr	Ala	His	Gly	Thr	Leu	Leu	Val	
				325					330					335		
Asn	Asp	Val	Leu	Ala	Ser	Cys	Tyr	Ala	Val	Leu	Glu	Ser	His	Gln	Trp	
			340					345					350			

Ala His Arg Ala Phe Ala Pro Leu Arg Leu Leu His Ala Leu Gly Ala
 355 360 365

Leu Leu Pro Gly Gly Ala Val Gln Pro Thr Gly Met His Trp Tyr Ser
 370 375 380

Arg Leu Leu Tyr Arg Leu Ala Glu Glu Leu Met Gly
 385 390 395

<210> 12

<211> 411

<212> PRT

<213> Murine sp.

<400> 12

Met Ser Pro Ala Trp Leu Arg Pro Arg Leu Arg Phe Cys Leu Phe Leu
 1 5 10 15

Leu Leu Leu Leu Leu Val Pro Ala Ala Arg Gly Cys Gly Pro Gly Arg
 20 25 30

Val Val Gly Ser Arg Arg Arg Pro Pro Arg Lys Leu Val Pro Leu Ala
 35 40 45

Tyr Lys Gln Phe Ser Pro Asn Val Pro Glu Lys Thr Leu Gly Ala Ser
 50 55 60

Gly Arg Tyr Glu Gly Lys Ile Ala Arg Ser Ser Glu Arg Phe Lys Glu
 65 70 75 80

Leu Thr Pro Asn Tyr Asn Pro Asp Ile Ile Phe Lys Asp Glu Glu Asn
 85 90 95

Thr Gly Ala Asp Arg Leu Met Thr Gln Arg Cys Lys Asp Arg Leu Asn
 100 105 110

Ser Leu Ala Ile Ser Val Met Asn Gln Trp Pro Gly Val Lys Leu Arg
 115 120 125

Val Thr Glu Gly Arg Asp Glu Asp Gly His His Ser Glu Glu Ser Leu
 130 135 140

His Tyr Glu Gly Arg Ala Val Asp Ile Thr Thr Ser Asp Arg Asp Arg
 145 150 155 160

Asn Lys Tyr Gly Leu Leu Ala Arg Leu Ala Val Glu Ala Gly Phe Asp
 165 170 175

Trp Val Tyr Tyr Glu Ser Lys Ala His Val His Cys Ser Val Lys Ser
 180 185 190

Glu His Ser Ala Ala Ala Lys Thr Gly Gly Cys Phe Pro Ala Gly Ala
 195 200 205

Gln Val Arg Leu Glu Asn Gly Glu Arg Val Ala Leu Ser Ala Val Lys
 210 215 220

Pro Gly Asp Arg Val Leu Ala Met Gly Glu Asp Gly Thr Pro Thr Phe
 225 230 235 240
 Ser Asp Val Leu Ile Phe Leu Asp Arg Glu Pro Asn Arg Leu Arg Ala
 245 250 255
 Phe Gln Val Ile Glu Thr Gln Asp Pro Pro Arg Arg Leu Ala Leu Thr
 260 265 270
 Pro Ala His Leu Leu Phe Ile Ala Asp Asn His Thr Glu Pro Ala Ala
 275 280 285
 His Phe Arg Ala Thr Phe Ala Ser His Val Gln Pro Gly Gln Tyr Val
 290 295 300
 Leu Val Ser Gly Val Pro Gly Leu Gln Pro Ala Arg Val Ala Ala Val
 305 310 315 320
 Ser Thr His Val Ala Leu Gly Ser Tyr Ala Pro Leu Thr Arg His Gly
 325 330 335
 Thr Leu Val Val Glu Asp Val Val Ala Ser Cys Phe Ala Ala Val Ala
 340 345 350
 Asp His His Leu Ala Gln Leu Ala Phe Trp Pro Leu Arg Leu Phe Pro
 355 360 365
 Ser Leu Ala Trp Gly Ser Trp Thr Pro Ser Glu Gly Val His Ser Tyr
 370 375 380
 Pro Gln Met Leu Tyr Arg Leu Gly Arg Leu Leu Leu Glu Glu Ser Thr
 385 390 395 400
 Phe His Pro Leu Gly Met Ser Gly Ala Gly Ser
 405 410

<210> 13
 <211> 437
 <212> PRT
 <213> Murine sp.

<400> 13
 Met Leu Leu Leu Leu Ala Arg Cys Phe Leu Val Ile Leu Ala Ser Ser
 1 5 10 15
 Leu Leu Val Cys Pro Gly Leu Ala Cys Gly Pro Gly Arg Gly Phe Gly
 20 25 30
 Lys Arg Arg His Pro Lys Lys Leu Thr Pro Leu Ala Tyr Lys Gln Phe
 35 40 45
 Ile Pro Asn Val Ala Glu Lys Thr Leu Gly Ala Ser Gly Arg Tyr Glu
 50 55 60
 Gly Lys Ile Thr Arg Asn Ser Glu Arg Phe Lys Glu Leu Thr Pro Asn
 65 70 75 80

Tyr	Asn	Pro	Asp	Ile 85	Ile	Phe	Lys	Asp	Glu 90	Glu	Asn	Thr	Gly	Ala 95	Asp
Arg	Leu	Met	Thr 100	Gln	Arg	Cys	Lys	Asp 105	Lys	Leu	Asn	Ala	Leu 110	Ala	Ile
Ser	Val	Met 115	Asn	Gln	Trp	Pro	Gly 120	Val	Arg	Leu	Arg	Val 125	Thr	Glu	Gly
Trp	Asp 130	Glu	Asp	Gly	His	His 135	Ser	Glu	Glu	Ser	Leu 140	His	Tyr	Glu	Gly
Arg 145	Ala	Val	Asp	Ile	Thr 150	Thr	Ser	Asp	Arg	Asp 155	Arg	Ser	Lys	Tyr	Gly 160
Met	Leu	Ala	Arg	Leu 165	Ala	Val	Glu	Ala	Gly 170	Phe	Asp	Trp	Val	Tyr 175	Tyr
Glu	Ser	Lys	Ala 180	His	Ile	His	Cys	Ser 185	Val	Lys	Ala	Glu	Asn 190	Ser	Val
Ala	Ala 195	Lys	Ser	Gly	Gly	Cys	Phe 200	Pro	Gly	Ser	Ala	Thr 205	Val	His	Leu
Glu	Gln 210	Gly	Gly	Thr	Lys	Leu 215	Val	Lys	Asp	Leu	Arg 220	Pro	Gly	Asp	Arg
Val 225	Leu	Ala	Ala	Asp	Asp 230	Gln	Gly	Arg	Leu	Leu 235	Tyr	Ser	Asp	Phe	Leu 240
Thr	Phe	Leu	Asp 245	Arg	Asp	Glu	Gly	Ala 250	Lys	Lys	Val	Phe	Tyr	Val 255	Ile
Glu	Thr	Leu	Glu 260	Pro	Arg	Glu	Arg	Leu 265	Leu	Leu	Thr	Ala	Ala 270	His	Leu
Leu	Phe	Val 275	Ala	Pro	His	Asn	Asp 280	Ser	Gly	Pro	Thr	Pro 285	Gly	Pro	Ser
Ala 290	Leu	Phe	Ala	Ser	Arg	Val 295	Arg	Pro	Gly	Gln	Arg 300	Val	Tyr	Val	Val
Ala 305	Glu	Arg	Gly	Gly	Asp 310	Arg	Arg	Leu	Leu	Pro 315	Ala	Ala	Val	His	Ser 320
Val	Thr	Leu	Arg	Glu 325	Glu	Glu	Ala	Gly	Ala 330	Tyr	Ala	Pro	Leu	Thr 335	Ala
His	Gly	Thr	Ile 340	Leu	Ile	Asn	Arg	Val 345	Leu	Ala	Ser	Cys	Tyr 350	Ala	Val
Ile	Glu	Glu 355	His	Ser	Trp	Ala	His 360	Arg	Ala	Phe	Ala	Pro 365	Phe	Arg	Leu
Ala	His 370	Ala	Leu	Leu	Ala	Ala 375	Leu	Ala	Pro	Ala	Arg 380	Thr	Asp	Gly	Gly

Gly Gly Gly Ser Ile Pro Ala Ala Gln Ser Ala Thr Glu Ala Arg Gly
385 390 395 400

Ala Glu Pro Thr Ala Gly Ile His Trp Tyr Ser Gln Leu Leu Tyr His
405 410 415

Ile Gly Thr Trp Leu Leu Asp Ser Glu Thr Met His Pro Leu Gly Met
420 425 430

Ala Val Lys Ser Ser
435

<210> 14

<211> 418

<212> PRT

<213> Brachydanio rerio

<400> 14

Met Arg Leu Leu Thr Arg Val Leu Leu Val Ser Leu Leu Thr Leu Ser
1 5 10 15

Leu Val Val Ser Gly Leu Ala Cys Gly Pro Gly Arg Gly Tyr Gly Arg
20 25 30

Arg Arg His Pro Lys Lys Leu Thr Pro Leu Ala Tyr Lys Gln Phe Ile
35 40 45

Pro Asn Val Ala Glu Lys Thr Leu Gly Ala Ser Gly Arg Tyr Glu Gly
50 55 60

Lys Ile Thr Arg Asn Ser Glu Arg Phe Lys Glu Leu Thr Pro Asn Tyr
65 70 75 80

Asn Pro Asp Ile Ile Phe Lys Asp Glu Glu Asn Thr Gly Ala Asp Arg
85 90 95

Leu Met Thr Gln Arg Cys Lys Asp Lys Leu Asn Ser Leu Ala Ile Ser
100 105 110

Val Met Asn His Trp Pro Gly Val Lys Leu Arg Val Thr Glu Gly Trp
115 120 125

Asp Glu Asp Gly His His Phe Glu Glu Ser Leu His Tyr Glu Gly Arg
130 135 140

Ala Val Asp Ile Thr Thr Ser Asp Arg Asp Lys Ser Lys Tyr Gly Thr
145 150 155 160

Leu Ser Arg Leu Ala Val Glu Ala Gly Phe Asp Trp Val Tyr Tyr Glu
165 170 175

Ser Lys Ala His Ile His Cys Ser Val Lys Ala Glu Asn Ser Val Ala
180 185 190

Ala Lys Ser Gly Gly Cys Phe Pro Gly Ser Ala Leu Val Ser Leu Gln
195 200 205

Asp Gly Gly Gln Lys Ala Val Lys Asp Leu Asn Pro Gly Asp Lys Val
 210 215 220
 Leu Ala Ala Asp Ser Ala Gly Asn Leu Val Phe Ser Asp Phe Ile Met
 225 230 235 240
 Phe Thr Asp Arg Asp Ser Thr Thr Arg Arg Val Phe Tyr Val Ile Glu
 245 250 255
 Thr Gln Glu Pro Val Glu Lys Ile Thr Leu Thr Ala Ala His Leu Leu
 260 265 270
 Phe Val Leu Asp Asn Ser Thr Glu Asp Leu His Thr Met Thr Ala Ala
 275 280 285
 Tyr Ala Ser Ser Val Arg Ala Gly Gln Lys Val Met Val Val Asp Asp
 290 295 300
 Ser Gly Gln Leu Lys Ser Val Ile Val Gln Arg Ile Tyr Thr Glu Glu
 305 310 315 320
 Gln Arg Gly Ser Phe Ala Pro Val Thr Ala His Gly Thr Ile Val Val
 325 330 335
 Asp Arg Ile Leu Ala Ser Cys Tyr Ala Val Ile Glu Asp Gln Gly Leu
 340 345 350
 Ala His Leu Ala Phe Ala Pro Ala Arg Leu Tyr Tyr Tyr Val Ser Ser
 355 360 365
 Phe Leu Ser Pro Lys Thr Pro Ala Val Gly Pro Met Arg Leu Tyr Asn
 370 375 380
 Arg Arg Gly Ser Thr Gly Thr Pro Gly Ser Cys His Gln Met Gly Thr
 385 390 395 400
 Trp Leu Leu Asp Ser Asn Met Leu His Pro Leu Gly Met Ser Val Asn
 405 410 415

Ser Ser

<210> 15

<211> 475

<212> PRT

<213> Homo sapien

<220>

<221> MOD_RES

<222> (463)

<223> any or unknown amino acid

<400> 15

Met Leu Leu Leu Ala Arg Cys Leu Leu Leu Val Leu Val Ser Ser Leu
 1 5 10 15

Leu Val Cys Ser Gly Leu Ala Cys Gly Pro Gly Arg Gly Phe Gly Lys
 20 25 30

Arg	Arg	His	Pro	Lys	Lys	Leu	Thr	Pro	Leu	Ala	Tyr	Lys	Gln	Phe	Ile	35	40	45	
Pro	Asn	Val	Ala	Glu	Lys	Thr	Leu	Gly	Ala	Ser	Gly	Arg	Tyr	Glu	Gly	50	55	60	
Lys	Ile	Ser	Arg	Asn	Ser	Glu	Arg	Phe	Lys	Glu	Leu	Thr	Pro	Asn	Tyr	65	70	75	80
Asn	Pro	Asp	Ile	Ile	Phe	Lys	Asp	Glu	Glu	Asn	Thr	Gly	Ala	Asp	Arg	85	90	95	
Leu	Met	Thr	Gln	Arg	Cys	Lys	Asp	Lys	Leu	Asn	Ala	Leu	Ala	Ile	Ser	100	105	110	
Val	Met	Asn	Gln	Trp	Pro	Gly	Val	Lys	Leu	Arg	Val	Thr	Glu	Gly	Trp	115	120	125	
Asp	Glu	Asp	Gly	His	His	Ser	Glu	Glu	Ser	Leu	His	Tyr	Glu	Gly	Arg	130	135	140	
Ala	Val	Asp	Ile	Thr	Thr	Ser	Asp	Arg	Asp	Arg	Ser	Lys	Tyr	Gly	Met	145	150	155	160
Leu	Ala	Arg	Leu	Ala	Val	Glu	Ala	Gly	Phe	Asp	Trp	Val	Tyr	Tyr	Glu	165	170	175	
Ser	Lys	Ala	His	Ile	His	Cys	Ser	Val	Lys	Ala	Glu	Asn	Ser	Val	Ala	180	185	190	
Ala	Lys	Ser	Gly	Gly	Cys	Phe	Pro	Gly	Ser	Ala	Thr	Val	His	Leu	Glu	195	200	205	
Gln	Gly	Gly	Thr	Lys	Leu	Val	Lys	Asp	Leu	Ser	Pro	Gly	Asp	Arg	Val	210	215	220	
Leu	Ala	Ala	Asp	Asp	Gln	Gly	Arg	Leu	Leu	Tyr	Ser	Asp	Phe	Leu	Thr	225	230	235	240
Phe	Leu	Asp	Arg	Asp	Asp	Gly	Ala	Lys	Lys	Val	Phe	Tyr	Val	Ile	Glu	245	250	255	
Thr	Arg	Glu	Pro	Arg	Glu	Arg	Leu	Leu	Leu	Thr	Ala	Ala	His	Leu	Leu	260	265	270	
Phe	Val	Ala	Pro	His	Asn	Asp	Ser	Ala	Thr	Gly	Glu	Pro	Glu	Ala	Ser	275	280	285	
Ser	Gly	Ser	Gly	Pro	Pro	Ser	Gly	Gly	Ala	Leu	Gly	Pro	Arg	Ala	Leu	290	295	300	
Phe	Ala	Ser	Arg	Val	Arg	Pro	Gly	Gln	Arg	Val	Tyr	Val	Val	Ala	Glu	305	310	315	320
Arg	Asp	Gly	Asp	Arg	Arg	Leu	Leu	Pro	Ala	Ala	Val	His	Ser	Val	Thr	325	330	335	

Leu Ser Glu Glu Ala Ala Gly Ala Tyr Ala Pro Leu Thr Ala Gln Gly
 340 345 350
 Thr Ile Leu Ile Asn Arg Val Leu Ala Ser Cys Tyr Ala Val Ile Glu
 355 360 365
 Glu His Ser Trp Ala His Arg Ala Phe Ala Pro Phe Arg Leu Ala His
 370 375 380
 Ala Leu Leu Ala Ala Leu Ala Pro Ala Arg Thr Asp Arg Gly Gly Asp
 385 390 395 400
 Ser Gly Gly Gly Asp Arg Gly Gly Gly Gly Gly Arg Val Ala Leu Thr
 405 410 415
 Ala Pro Gly Ala Ala Asp Ala Pro Gly Ala Gly Ala Thr Ala Gly Ile
 420 425 430
 His Trp Tyr Ser Gln Leu Leu Tyr Gln Ile Gly Thr Trp Leu Leu Asp
 435 440 445
 Ser Glu Ala Leu His Pro Leu Gly Met Ala Val Lys Ser Ser Xaa Ser
 450 455 460
 Arg Gly Ala Gly Gly Gly Ala Arg Glu Gly Ala
 465 470 475

<210> 16
 <211> 411
 <212> PRT
 <213> Homo sapien

<400> 16
 Met Ser Pro Ala Arg Leu Arg Pro Arg Leu His Phe Cys Leu Val Leu
 1 5 10 15
 Leu Leu Leu Leu Val Val Pro Ala Ala Trp Gly Cys Gly Pro Gly Arg
 20 25 30
 Val Val Gly Ser Arg Arg Arg Pro Pro Arg Lys Leu Val Pro Leu Ala
 35 40 45
 Tyr Lys Gln Phe Ser Pro Asn Val Pro Glu Lys Thr Leu Gly Ala Ser
 50 55 60
 Gly Arg Tyr Glu Gly Lys Ile Ala Arg Ser Ser Glu Arg Phe Lys Glu
 65 70 75 80
 Leu Thr Pro Asn Tyr Asn Pro Asp Ile Ile Phe Lys Asp Glu Glu Asn
 85 90 95
 Thr Gly Ala Asp Arg Leu Met Thr Gln Arg Cys Lys Asp Arg Leu Asn
 100 105 110
 Ser Leu Ala Ile Ser Val Met Asn Gln Trp Pro Gly Val Lys Leu Arg
 115 120 125

Val	Thr	Glu	Gly	Trp	Asp	Glu	Asp	Gly	His	His	Ser	Glu	Glu	Ser	Leu	130	135	140
His	Tyr	Glu	Gly	Arg	Ala	Val	Asp	Ile	Thr	Thr	Ser	Asp	Arg	Asp	Arg	145	150	155
Asn	Lys	Tyr	Gly	Leu	Leu	Ala	Arg	Leu	Ala	Val	Glu	Ala	Gly	Phe	Asp	165	170	175
Trp	Val	Tyr	Tyr	Glu	Ser	Lys	Ala	His	Val	His	Cys	Ser	Val	Lys	Ser	180	185	190
Glu	His	Ser	Ala	Ala	Ala	Lys	Thr	Gly	Gly	Cys	Phe	Pro	Ala	Gly	Ala	195	200	205
Gln	Val	Arg	Leu	Glu	Ser	Gly	Ala	Arg	Val	Ala	Leu	Ser	Ala	Val	Arg	210	215	220
Pro	Gly	Asp	Arg	Val	Leu	Ala	Met	Gly	Glu	Asp	Gly	Ser	Pro	Thr	Phe	225	230	235
Ser	Asp	Val	Leu	Ile	Phe	Leu	Asp	Arg	Glu	Pro	His	Arg	Leu	Arg	Ala	245	250	255
Phe	Gln	Val	Ile	Glu	Thr	Gln	Asp	Pro	Pro	Arg	Arg	Leu	Ala	Leu	Thr	260	265	270
Pro	Ala	His	Leu	Leu	Phe	Thr	Ala	Asp	Asn	His	Thr	Glu	Pro	Ala	Ala	275	280	285
Arg	Phe	Arg	Ala	Thr	Phe	Ala	Ser	His	Val	Gln	Pro	Gly	Gln	Tyr	Val	290	295	300
Leu	Val	Ala	Gly	Val	Pro	Gly	Leu	Gln	Pro	Ala	Arg	Val	Ala	Ala	Val	305	310	315
Ser	Thr	His	Val	Ala	Leu	Gly	Ala	Tyr	Ala	Pro	Leu	Thr	Lys	His	Gly	325	330	335
Thr	Leu	Val	Val	Glu	Asp	Val	Val	Ala	Ser	Cys	Phe	Ala	Ala	Val	Ala	340	345	350
Asp	His	His	Leu	Ala	Gln	Leu	Ala	Phe	Trp	Pro	Leu	Arg	Leu	Phe	His	355	360	365
Ser	Leu	Ala	Trp	Gly	Ser	Trp	Thr	Pro	Gly	Glu	Gly	Val	His	Trp	Tyr	370	375	380
Pro	Gln	Leu	Leu	Tyr	Arg	Leu	Gly	Arg	Leu	Leu	Leu	Glu	Glu	Gly	Ser	385	390	395
Phe	His	Pro	Leu	Gly	Met	Ser	Gly	Ala	Gly	Ser						405	410	

<210> 17
 <211> 396
 <212> PRT
 <213> Homo sapien

<400> 17

Met	Ala	Leu	Leu	Thr	Asn	Leu	Leu	Pro	Leu	Cys	Cys	Leu	Ala	Leu	Leu
1				5					10					15	
Ala	Leu	Pro	Ala	Gln	Ser	Cys	Gly	Pro	Gly	Arg	Gly	Pro	Val	Gly	Arg
			20					25					30		
Arg	Arg	Tyr	Ala	Arg	Lys	Gln	Leu	Val	Pro	Leu	Leu	Tyr	Lys	Gln	Phe
		35					40					45			
Val	Pro	Gly	Val	Pro	Glu	Arg	Thr	Leu	Gly	Ala	Ser	Gly	Pro	Ala	Glu
	50					55					60				
Gly	Arg	Val	Ala	Arg	Gly	Ser	Glu	Arg	Phe	Arg	Asp	Leu	Val	Pro	Asn
65					70					75					80
Tyr	Asn	Pro	Asp	Ile	Ile	Phe	Lys	Asp	Glu	Glu	Asn	Ser	Gly	Ala	Asp
				85					90					95	
Arg	Leu	Met	Thr	Glu	Arg	Cys	Lys	Glu	Arg	Val	Asn	Ala	Leu	Ala	Ile
			100					105					110		
Ala	Val	Met	Asn	Met	Trp	Pro	Gly	Val	Arg	Leu	Arg	Val	Thr	Glu	Gly
		115					120					125			
Trp	Asp	Glu	Asp	Gly	His	His	Ala	Gln	Asp	Ser	Leu	His	Tyr	Glu	Gly
	130					135					140				
Arg	Ala	Leu	Asp	Ile	Thr	Thr	Ser	Asp	Arg	Asp	Arg	Asn	Lys	Tyr	Gly
145					150					155					160
Leu	Leu	Ala	Arg	Leu	Ala	Val	Glu	Ala	Gly	Phe	Asp	Trp	Val	Tyr	Tyr
				165					170					175	
Glu	Ser	Arg	Asn	His	Val	His	Val	Ser	Val	Lys	Ala	Asp	Asn	Ser	Leu
			180					185					190		
Ala	Val	Arg	Ala	Gly	Gly	Cys	Phe	Pro	Gly	Asn	Ala	Thr	Val	Arg	Leu
		195					200					205			
Trp	Ser	Gly	Glu	Arg	Lys	Gly	Leu	Arg	Glu	Leu	His	Arg	Gly	Asp	Trp
	210					215					220				
Val	Leu	Ala	Ala	Asp	Ala	Ser	Gly	Arg	Val	Val	Pro	Thr	Pro	Val	Leu
225					230					235					240
Leu	Phe	Leu	Asp	Arg	Asp	Leu	Gln	Arg	Arg	Ala	Ser	Phe	Val	Ala	Val
				245					250					255	
Glu	Thr	Glu	Trp	Pro	Pro	Arg	Lys	Leu	Leu	Leu	Thr	Pro	Trp	His	Leu
			260					265					270		
Val	Phe	Ala	Ala	Arg	Gly	Pro	Ala	Pro	Ala	Pro	Gly	Asp	Phe	Ala	Pro
		275					280					285			
Val	Phe	Ala	Arg	Arg	Leu	Arg	Ala	Gly	Asp	Ser	Val	Leu	Ala	Pro	Gly
						295					300				

Gly Asp Ala Leu Arg Pro Ala Arg Val Ala Arg Val Ala Arg Glu Glu
305 310 315 320

Ala Val Gly Val Phe Ala Pro Leu Thr Ala His Gly Thr Leu Leu Val
325 330 335

Asn Asp Val Leu Ala Ser Cys Tyr Ala Val Leu Glu Ser His Gln Trp
340 345 350

Ala His Arg Ala Phe Ala Pro Leu Arg Leu Leu His Ala Leu Gly Ala
355 360 365

Leu Leu Pro Gly Gly Ala Val Gln Pro Thr Gly Met His Trp Tyr Ser
370 375 380

Arg Leu Leu Tyr Arg Leu Ala Glu Glu Leu Leu Gly
385 390 395

<210> 18

<211> 416

<212> PRT

<213> Brachydanio rerio

<400> 18

Met Asp Val Arg Leu His Leu Lys Gln Phe Ala Leu Leu Cys Phe Ile
1 5 10 15

Ser Leu Leu Leu Thr Pro Cys Gly Leu Ala Cys Gly Pro Gly Arg Gly
20 25 30

Tyr Gly Lys Arg Arg His Pro Lys Lys Leu Thr Pro Leu Ala Tyr Lys
35 40 45

Gln Phe Ile Pro Asn Val Ala Glu Lys Thr Leu Gly Ala Ser Gly Lys
50 55 60

Tyr Glu Gly Lys Ile Thr Arg Asn Ser Glu Arg Phe Lys Glu Leu Ile
65 70 75 80

Pro Asn Tyr Asn Pro Asp Ile Ile Phe Lys Asp Glu Glu Asn Thr Asn
85 90 95

Ala Asp Arg Leu Met Thr Lys Arg Cys Lys Asp Lys Leu Asn Ser Leu
100 105 110

Ala Ile Ser Val Met Asn His Trp Pro Gly Val Lys Leu Arg Val Thr
115 120 125

Glu Gly Trp Asp Glu Asp Gly His His Leu Glu Glu Ser Leu His Tyr
130 135 140

Glu Gly Arg Ala Val Asp Ile Thr Thr Ser Asp Arg Asp Lys Ser Lys
145 150 155 160

Tyr Gly Met Leu Ser Arg Leu Ala Val Glu Ala Gly Phe Asp Trp Val
165 170 175

Tyr Tyr Glu Ser Lys Ala His Ile His Cys Ser Val Lys Ala Glu Asn
 180 185 190
 Ser Val Ala Ala Lys Ser Gly Gly Cys Phe Pro Gly Ser Gly Thr Val
 195 200 205
 Thr Leu Gly Asp Gly Thr Arg Lys Pro Ile Lys Asp Leu Lys Val Gly
 210 215 220
 Asp Arg Val Leu Ala Ala Asp Glu Lys Gly Asn Val Leu Ile Ser Asp
 225 230 235 240
 Phe Ile Met Phe Ile Asp His Asp Pro Thr Thr Arg Arg Gln Phe Ile
 245 250 255
 Val Ile Glu Thr Ser Glu Pro Phe Thr Lys Leu Thr Leu Thr Ala Ala
 260 265 270
 His Leu Val Phe Val Gly Asn Ser Ser Ala Ala Ser Gly Ile Thr Ala
 275 280 285
 Thr Phe Ala Ser Asn Val Lys Pro Gly Asp Thr Val Leu Val Trp Glu
 290 295 300
 Asp Thr Cys Glu Ser Leu Lys Ser Val Thr Val Lys Arg Ile Tyr Thr
 305 310 315 320
 Glu Glu His Glu Gly Ser Phe Ala Pro Val Thr Ala His Gly Thr Ile
 325 330 335
 Ile Val Asp Gln Val Leu Ala Ser Cys Tyr Ala Val Ile Glu Asn His
 340 345 350
 Lys Trp Ala His Trp Ala Phe Ala Pro Val Arg Leu Cys His Lys Leu
 355 360 365
 Met Thr Trp Leu Phe Pro Ala Arg Glu Ser Asn Val Asn Phe Gln Glu
 370 375 380
 Asp Gly Ile His Trp Tyr Ser Asn Met Leu Phe His Ile Gly Ser Trp
 385 390 395 400
 Leu Leu Asp Arg Asp Ser Phe His Pro Leu Gly Ile Leu His Leu Ser
 405 410 415

<210> 19

<211> 1416

<212> DNA

<213> Drosophila sp.

<220>

<221> CDS

<222> (1)..(1413)

<400> 19

atg gat aac cac agc tca gtg cct tgg gcc agt gcc gcc agt gtc acc
 Met Asp Asn His Ser Ser Val Pro Trp Ala Ser Ala Ala Ser Val Thr
 1 5 10 15

tgt	ctc	tcc	ctg	gga	tgc	caa	atg	cca	cag	ttc	cag	ttc	cag	ttc	cag	96
Cys	Leu	Ser	Leu	Gly	Cys	Gln	Met	Pro	Gln	Phe	Gln	Phe	Gln	Phe	Gln	
			20					25					30			
ctc	caa	atc	cgc	agc	gag	ctc	cat	ctc	cgc	aag	ccc	gca	aga	aga	acg	144
Leu	Gln	Ile	Arg	Ser	Glu	Leu	His	Leu	Arg	Lys	Pro	Ala	Arg	Arg	Thr	
		35					40					45				
caa	acg	atg	cgc	cac	att	gcg	cat	acg	cag	cgt	tgc	ctc	agc	agg	ctg	192
Gln	Thr	Met	Arg	His	Ile	Ala	His	Thr	Gln	Arg	Cys	Leu	Ser	Arg	Leu	
	50					55					60					
acc	tct	ctg	gtg	gcc	ctg	ctg	ctg	atc	gtc	ttg	ccg	atg	gtc	ttt	agc	240
Thr	Ser	Leu	Val	Ala	Leu	Leu	Leu	Ile	Val	Leu	Pro	Met	Val	Phe	Ser	
	65				70				75						80	
ccg	gct	cac	agc	tgc	ggg	cct	ggc	cga	gga	ttg	ggg	cgt	cat	agg	gcg	288
Pro	Ala	His	Ser	Cys	Gly	Pro	Gly	Arg	Gly	Leu	Gly	Arg	His	Arg	Ala	
			85					90						95		
cgc	aac	ctg	tat	ccg	ctg	gtc	ctc	aag	cag	aca	att	ccc	aat	cta	tcc	336
Arg	Asn	Leu	Tyr	Pro	Leu	Val	Leu	Lys	Gln	Thr	Ile	Pro	Asn	Leu	Ser	
		100						105					110			
gag	tac	acg	aac	agc	gcc	tcc	gga	cct	ctg	gag	ggg	gtg	atc	cgt	cgg	384
Glu	Tyr	Thr	Asn	Ser	Ala	Ser	Gly	Pro	Leu	Glu	Gly	Val	Ile	Arg	Arg	
		115					120					125				
gat	tcg	ccc	aaa	ttc	aag	gac	ctc	gtg	ccc	aac	tac	aac	agg	gac	atc	432
Asp	Ser	Pro	Lys	Phe	Lys	Asp	Leu	Val	Pro	Asn	Tyr	Asn	Arg	Asp	Ile	
	130					135					140					
ctt	ttc	cgt	gac	gag	gaa	ggc	acc	gga	gcg	gat	ggc	ttg	atg	agc	aag	480
Leu	Phe	Arg	Asp	Glu	Glu	Gly	Thr	Gly	Ala	Asp	Gly	Leu	Met	Ser	Lys	
	145				150				155						160	
cgc	tgc	aag	gag	aag	cta	aac	gtg	ctg	gcc	tac	tcg	gtg	atg	aac	gaa	528
Arg	Cys	Lys	Glu	Lys	Leu	Asn	Val	Leu	Ala	Tyr	Ser	Val	Met	Asn	Glu	
			165					170						175		
tgg	ccc	ggc	atc	cgg	ctg	ctg	gtc	acc	gag	agc	tgg	gac	gag	gac	tac	576
Trp	Pro	Gly	Ile	Arg	Leu	Leu	Val	Thr	Glu	Ser	Trp	Asp	Glu	Asp	Tyr	
		180					185						190			
cat	cac	ggc	cag	gag	tcg	ctc	cac	tac	gag	ggc	cga	gcg	gtg	acc	att	624
His	His	Gly	Gln	Glu	Ser	Leu	His	Tyr	Glu	Gly	Arg	Ala	Val	Thr	Ile	
		195					200					205				
gcc	acc	tcc	gat	cgc	gac	cag	tcc	aaa	tac	ggc	atg	ctc	gct	cgc	ctg	672
Ala	Thr	Ser	Asp	Arg	Asp	Gln	Ser	Lys	Tyr	Gly	Met	Leu	Ala	Arg	Leu	
	210					215					220					
gcc	gtc	gag	gct	gga	ttc	gat	tgg	gtc	tcc	tac	gtc	agc	agg	cgc	cac	720
Ala	Val	Glu	Ala	Gly	Phe	Asp	Trp	Val	Ser	Tyr	Val	Ser	Arg	Arg	His	
	225				230				235						240	

atc tac tgc tcc gtc aag tca gat tcg tcg atc agt tcc cac gtg cac	768
Ile Tyr Cys Ser Val Lys Ser Asp Ser Ser Ile Ser Ser His Val His	
245 250 255	
ggc tgc ttc acg ccg gag agc aca gcg ctg ctg gag agt gga gtc cgg	816
Gly Cys Phe Thr Pro Glu Ser Thr Ala Leu Leu Glu Ser Gly Val Arg	
260 265 270	
aag ccg ctc ggc gag ctc tct atc gga gat cgt gtt ttg agc atg acc	864
Lys Pro Leu Gly Glu Leu Ser Ile Gly Asp Arg Val Leu Ser Met Thr	
275 280 285	
gcc aac gga cag gcc gtc tac agc gaa gtg atc ctc ttc atg gac cgc	912
Ala Asn Gly Gln Ala Val Tyr Ser Glu Val Ile Leu Phe Met Asp Arg	
290 295 300	
aac ctc gag cag atg caa aac ttt gtg cag ctg cac acg gac ggt gga	960
Asn Leu Glu Gln Met Gln Asn Phe Val Gln Leu His Thr Asp Gly Gly	
305 310 315 320	
gca gtg ctc acg gtg acg ccg gct cac ctg gtt agc gtt tgg cag ccg	1008
Ala Val Leu Thr Val Thr Pro Ala His Leu Val Ser Val Trp Gln Pro	
325 330 335	
gag agc cag aag ctc acg ttt gtg ttt gcg cat cgc atc gag gag aag	1056
Glu Ser Gln Lys Leu Thr Phe Val Phe Ala His Arg Ile Glu Glu Lys	
340 345 350	
aac cag gtg ctc gta cgg gat gtg gag acg ggc gag ctg agg ccc cag	1104
Asn Gln Val Leu Val Arg Asp Val Glu Thr Gly Glu Leu Arg Pro Gln	
355 360 365	
cga gtg gtc aag ttg ggc agt gtg cgc agt aag ggc gtg gtc gcg ccg	1152
Arg Val Val Lys Leu Gly Ser Val Arg Ser Lys Gly Val Val Ala Pro	
370 375 380	
ctg acc cgc gag ggc acc att gtg gtc aac tcg gtg gcc gcc agt tgc	1200
Leu Thr Arg Glu Gly Thr Ile Val Val Asn Ser Val Ala Ala Ser Cys	
385 390 395 400	
tat gcg gtg atc aac agt cag tcg ctg gcc cac tgg gga ctg gct ccc	1248
Tyr Ala Val Ile Asn Ser Gln Ser Leu Ala His Trp Gly Leu Ala Pro	
405 410 415	
atg cgc ctg ctg tcc acg ctg gag gcg tgg ctg ccc gcc aag gag cag	1296
Met Arg Leu Leu Ser Thr Leu Glu Ala Trp Leu Pro Ala Lys Glu Gln	
420 425 430	
ttg cac agt tcg ccg aag gtg gtg agc tcg gcg cag cag cag aat ggc	1344
Leu His Ser Ser Pro Lys Val Val Ser Ser Ala Gln Gln Gln Asn Gly	
435 440 445	
atc cat tgg tat gcc aat gcg ctc tac aag gtc aag gac tac gtg ctg	1392
Ile His Trp Tyr Ala Asn Ala Leu Tyr Lys Val Lys Asp Tyr Val Leu	
450 455 460	

ccg cag agc tgg cgc cac gat tga
 Pro Gln Ser Trp Arg His Asp
 465 470

1416

<210> 20
 <211> 471
 <212> PRT
 <213> Drosophila sp.

<400> 20
 Met Asp Asn His Ser Ser Val Pro Trp Ala Ser Ala Ala Ser Val Thr
 1 5 10 15
 Cys Leu Ser Leu Gly Cys Gln Met Pro Gln Phe Gln Phe Gln Phe Gln
 20 25 30
 Leu Gln Ile Arg Ser Glu Leu His Leu Arg Lys Pro Ala Arg Arg Thr
 35 40 45
 Gln Thr Met Arg His Ile Ala His Thr Gln Arg Cys Leu Ser Arg Leu
 50 55 60
 Thr Ser Leu Val Ala Leu Leu Leu Ile Val Leu Pro Met Val Phe Ser
 65 70 75 80
 Pro Ala His Ser Cys Gly Pro Gly Arg Gly Leu Gly Arg His Arg Ala
 85 90 95
 Arg Asn Leu Tyr Pro Leu Val Leu Lys Gln Thr Ile Pro Asn Leu Ser
 100 105 110
 Glu Tyr Thr Asn Ser Ala Ser Gly Pro Leu Glu Gly Val Ile Arg Arg
 115 120 125
 Asp Ser Pro Lys Phe Lys Asp Leu Val Pro Asn Tyr Asn Arg Asp Ile
 130 135 140
 Leu Phe Arg Asp Glu Glu Gly Thr Gly Ala Asp Gly Leu Met Ser Lys
 145 150 155 160
 Arg Cys Lys Glu Lys Leu Asn Val Leu Ala Tyr Ser Val Met Asn Glu
 165 170 175
 Trp Pro Gly Ile Arg Leu Leu Val Thr Glu Ser Trp Asp Glu Asp Tyr
 180 185 190
 His His Gly Gln Glu Ser Leu His Tyr Glu Gly Arg Ala Val Thr Ile
 195 200 205
 Ala Thr Ser Asp Arg Asp Gln Ser Lys Tyr Gly Met Leu Ala Arg Leu
 210 215 220
 Ala Val Glu Ala Gly Phe Asp Trp Val Ser Tyr Val Ser Arg Arg His
 225 230 235 240
 Ile Tyr Cys Ser Val Lys Ser Asp Ser Ser Ile Ser Ser His Val His
 245 250 255

Gly Cys Phe Thr Pro Glu Ser Thr Ala Leu Leu Glu Ser Gly Val Arg
 260 265 270
 Lys Pro Leu Gly Glu Leu Ser Ile Gly Asp Arg Val Leu Ser Met Thr
 275 280 285
 Ala Asn Gly Gln Ala Val Tyr Ser Glu Val Ile Leu Phe Met Asp Arg
 290 295 300
 Asn Leu Glu Gln Met Gln Asn Phe Val Gln Leu His Thr Asp Gly Gly
 305 310 315 320
 Ala Val Leu Thr Val Thr Pro Ala His Leu Val Ser Val Trp Gln Pro
 325 330 335
 Glu Ser Gln Lys Leu Thr Phe Val Phe Ala His Arg Ile Glu Glu Lys
 340 345 350
 Asn Gln Val Leu Val Arg Asp Val Glu Thr Gly Glu Leu Arg Pro Gln
 355 360 365
 Arg Val Val Lys Leu Gly Ser Val Arg Ser Lys Gly Val Val Ala Pro
 370 375 380
 Leu Thr Arg Glu Gly Thr Ile Val Val Asn Ser Val Ala Ala Ser Cys
 385 390 395 400
 Tyr Ala Val Ile Asn Ser Gln Ser Leu Ala His Trp Gly Leu Ala Pro
 405 410 415
 Met Arg Leu Leu Ser Thr Leu Glu Ala Trp Leu Pro Ala Lys Glu Gln
 420 425 430
 Leu His Ser Ser Pro Lys Val Val Ser Ser Ala Gln Gln Gln Asn Gly
 435 440 445
 Ile His Trp Tyr Ala Asn Ala Leu Tyr Lys Val Lys Asp Tyr Val Leu
 450 455 460
 Pro Gln Ser Trp Arg His Asp
 465 470

<210> 21

<211> 221

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: degenerate
polypeptide sequence

<220>

<221> MOD_RES

<222> 7

<223> Gly, Ala, Val, Leu, Ile, Phe, Tyr or Trp

<220>
<221> MOD_RES
<222> 9
<223> Arg, His or Lys

<220>
<221> MOD_RES
<222> 44
<223> Gly, Ala, Val, Leu, Ile, Ser or Thr

<220>
<221> MOD_RES
<222> 85
<223> Gly, Ala, Val, Leu, Ile, Ser or Thr

<220>
<221> MOD_RES
<222> 93
<223> Lys, Arg, His, Asn or Gln

<220>
<221> MOD_RES
<222> 98
<223> Lys, Arg or His

<220>
<221> MOD_RES
<222> 112
<223> Ser, Thr, Tyr, Trp or Phe

<220>
<221> MOD_RES
<222> 132
<223> Lys, Arg or His

<220>
<221> MOD_RES
<222> 137
<223> Met, Cys, Ser or Thr

<220>
<221> MOD_RES
<222> 139
<223> Gly, Ala, Val, Leu, Ile, Ser or Thr

<220>
<221> MOD_RES
<222> 181
<223> Leu, Val, Met, Thr or Ser

<220>
<221> MOD_RES
<222> 183
<223> His, Phe, Tyr, Ser, Thr, Met or Cys

<220>
<221> MOD_RES
<222> 185

<223> Gln, Asn, Glu, or Asp

<220>
<221> MOD_RES
<222> 186
<223> His, Phe, Tyr, Thr, Gln, Asn, Glu or Asp

<220>
<221> MOD_RES
<222> 189
<223> Gln, Asn, Glu, Asp, Thr, Ser, Met or Cys

<220>
<221> MOD_RES
<222> 191
<223> Ala, Gly, Cys, Leu, Val or Met

<220>
<221> MOD_RES
<222> 196
<223> Arg, Lys, Met, Ile, Asn, Asp, Glu, Gln, Ser, Thr or Cys

<220>
<221> MOD_RES
<222> 200
<223> Arg, Lys, Met or Ile

<220>
<221> MOD_RES
<222> 206
<223> Ala, Gly, Cys, Asp, Glu, Gln, Asn, Ser, Thr or Met

<220>
<221> MOD_RES
<222> 207
<223> Ala, Gly, Cys, Asp, Asn, Glu or Gln

<220>
<221> MOD_RES
<222> 209
<223> Arg, Lys, Met, Ile, Asn, Asp, Glu or Gln

<220>
<221> MOD_RES
<222> 211
<223> Leu, Val, Met or Ile

<220>
<221> MOD_RES
<222> 212
<223> Phe, Tyr, Thr, His or Trp

<220>
<221> MOD_RES
<222> 216
<223> Ile, Val, Leu or Met

<220>

<221> MOD_RES

<222> 217

<223> Met, Cys, Ile, Leu, Val, Thr or Ser

<220>

<221> MOD_RES

<222> 219

<223> Leu, Val, Met, Thr or Ser

<220>

<223> each Xaa may also be any amino acid.

<400> 21

Cys	Gly	Pro	Gly	Arg	Gly	Xaa	Gly	Xaa	Arg	Arg	His	Pro	Lys	Lys	Leu
1				5					10					15	

Thr	Pro	Leu	Ala	Tyr	Lys	Gln	Phe	Ile	Pro	Asn	Val	Ala	Glu	Lys	Thr
			20					25					30		

Leu	Gly	Ala	Ser	Gly	Arg	Tyr	Glu	Gly	Lys	Ile	Xaa	Arg	Asn	Ser	Glu
		35					40					45			

Arg	Phe	Lys	Glu	Leu	Thr	Pro	Asn	Tyr	Asn	Pro	Asp	Ile	Ile	Phe	Lys
	50					55					60				

Asp	Glu	Glu	Asn	Thr	Gly	Ala	Asp	Arg	Leu	Met	Thr	Gln	Arg	Cys	Lys
65					70					75					80

Asp	Lys	Leu	Asn	Xaa	Leu	Ala	Ile	Ser	Val	Met	Asn	Xaa	Trp	Pro	Gly
			85						90					95	

Val	Xaa	Leu	Arg	Val	Thr	Glu	Gly	Trp	Asp	Glu	Asp	Gly	His	His	Xaa
		100						105					110		

Glu	Glu	Ser	Leu	His	Tyr	Glu	Gly	Arg	Ala	Val	Asp	Ile	Thr	Thr	Ser
		115					120					125			

Asp	Arg	Asp	Xaa	Ser	Lys	Tyr	Gly	Xaa	Leu	Xaa	Arg	Leu	Ala	Val	Glu
	130					135					140				

Ala	Gly	Phe	Asp	Trp	Val	Tyr	Tyr	Glu	Ser	Lys	Ala	His	Ile	His	Cys
145					150					155					160

Ser	Val	Lys	Ala	Glu	Asn	Ser	Val	Ala	Ala	Lys	Ser	Gly	Gly	Cys	Phe
			165						170					175	

Pro	Gly	Ser	Ala	Xaa	Val	Xaa	Leu	Xaa	Xaa	Gly	Gly	Xaa	Lys	Xaa	Val
			180					185					190		

Lys	Asp	Leu	Xaa	Pro	Gly	Asp	Xaa	Val	Leu	Ala	Ala	Asp	Xaa	Xaa	Gly
		195				200						205			

Xaa	Leu	Xaa	Xaa	Ser	Asp	Phe	Xaa	Xaa	Phe	Xaa	Asp	Arg
	210					215					220	

<210> 22

<211> 167

<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: degenerate
polypeptide sequence

<220>
<221> MOD_RES
<222> 7
<223> Gly, Ala, Val, Leu, Ile, Pro, Phe or Tyr

<220>
<221> MOD_RES
<222> 8
<223> Gly, Ala, Val, Leu or Ile

<220>
<221> MOD_RES
<222> 9
<223> Gly, Ala, Val, Leu, Ile, Lys, His or Arg

<220>
<221> MOD_RES
<222> 12
<223> Lys, Arg or His

<220>
<221> MOD_RES
<222> 13
<223> Phe, Trp, Tyr or an amino acid gap

<220>
<221> MOD_RES
<222> 14
<223> Gly, Ala, Val, Leu, Ile or an amino acid gap

<220>
<221> MOD_RES
<222> 17
<223> Asn, Gln, His, Arg or Lys

<220>
<221> MOD_RES
<222> 19
<223> Gly, Ala, Val, Leu, Ile, Ser or Thr

<220>
<221> MOD_RES
<222> 22
<223> Gly, Ala, Val, Leu, Ile, Ser or Thr

<220>
<221> MOD_RES
<222> 27
<223> Gly, Ala, Val, Leu, Ile, Ser or Thr

<220>

<221> MOD_RES
<222> 29
<223> Ser, Thr, Gln or Asn

<220>
<221> MOD_RES
<222> 30
<223> Met, Cys, Gly, Ala, Val, Leu, Ile, Ser or Thr

<220>
<221> MOD_RES
<222> 31
<223> Gly, Ala, Val, Leu, Ile or Pro

<220>
<221> MOD_RES
<222> 33
<223> Arg, His or Lys

<220>
<221> MOD_RES
<222> 40
<223> Gly, Ala, Val, Leu, Ile, Pro, Arg, His or Lys

<220>
<221> MOD_RES
<222> 41
<223> Gly, Ala, Val, Leu, Ile, Phe or Tyr

<220>
<221> MOD_RES
<222> 44
<223> Arg, His or Lys

<220>
<221> MOD_RES
<222> 45
<223> Gly, Ala, Val, Leu, Ile, Ser or Thr

<220>
<221> MOD_RES
<222> 46
<223> Thr or Ser

<220>
<221> MOD_RES
<222> 48
<223> Gly, Ala, Val, Leu, Ile, Asn or Gln

<220>
<221> MOD_RES
<222> 53
<223> Arg, His or Lys

<220>
<221> MOD_RES
<222> 54
<223> Asp or Glu

<220>
<221> MOD_RES
<222> 71
<223> Ser or Thr

<220>
<221> MOD_RES
<222> 79
<223> Glu, Asp, Gln or Asn

<220>
<221> MOD_RES
<222> 83
<223> Glu or Asp

<220>
<221> MOD_RES
<222> 84
<223> Arg, His or Lys

<220>
<221> MOD_RES
<222> 85
<223> Gly, Ala, Val, Leu or Ile

<220>
<221> MOD_RES
<222> 87
<223> Gly, Ala, Val, Leu, Ile, Thr or Ser

<220>
<221> MOD_RES
<222> 95
<223> Met, Cys, Gln, Asn, Arg, Lys or His

<220>
<221> MOD_RES
<222> 100
<223> Arg, His or Lys

<220>
<221> MOD_RES
<222> 107
<223> Trp, Phe, Tyr, Arg, His or Lys

<220>
<221> MOD_RES
<222> 114
<223> Gly, Ala, Val, Leu, Ile, Ser, Thr, Tyr or Phe

<220>
<221> MOD_RES
<222> 115
<223> Gln, Asn, Asp or Glu

<220>
<221> MOD_RES

<222> 116
<223> Asp or Glu

<220>
<221> MOD_RES
<222> 125
<223> Gly, Ala, Val, Leu, or Ile

<220>
<221> MOD_RES
<222> 134
<223> Arg, His or Lys

<220>
<221> MOD_RES
<222> 135
<223> Asn, Gln, Thr or Ser

<220>
<221> MOD_RES
<222> 139
<223> Gly, Ala, Val, Leu, Ile, Ser, Thr, Met or Cys

<220>
<221> MOD_RES
<222> 141
<223> Gly, Ala, Val, Leu, Ile, Thr or Ser

<220>
<221> MOD_RES
<222> 157
<223> Arg, His or Lys

<220>
<221> MOD_RES
<222> 158
<223> Asn, Gln, Gly, Ala, Val, Leu or Ile

<220>
<221> MOD_RES
<222> 160
<223> Gly, Ala, Val, Leu or Ile

<220>
<221> MOD_RES
<222> 162
<223> Gly, Ala, Val, Leu, Ile, Ser, Thr or Cys

<220>
<221> MOD_RES
<222> 166
<223> Gly, Ala, Val, Leu, Ile, Thr or Ser

<220>
<221> MOD_RES
<222> 167
<223> Asp or Glu

<400> 22

Cys Gly Pro Gly Arg Gly Xaa Xaa Xaa Arg Arg Xaa Xaa Xaa Pro Lys
 1 5 10 15

Xaa Leu Xaa Pro Leu Xaa Tyr Lys Gln Phe Xaa Pro Xaa Xaa Xaa Glu
 20 25 30

Xaa Thr Leu Gly Ala Ser Gly Xaa Xaa Glu Gly Xaa Xaa Xaa Arg Xaa
 35 40 45

Ser Glu Arg Phe Xaa Xaa Leu Thr Pro Asn Tyr Asn Pro Asp Ile Ile
 50 55 60

Phe Lys Asp Glu Glu Asn Xaa Gly Ala Asp Arg Leu Met Thr Xaa Arg
 65 70 75 80

Cys Lys Xaa Xaa Xaa Asn Xaa Leu Ala Ile Ser Val Met Asn Xaa Trp
 85 90 95

Pro Gly Val Xaa Leu Arg Val Thr Glu Gly Xaa Asp Glu Asp Gly His
 100 105 110

His Xaa Xaa Xaa Ser Leu His Tyr Glu Gly Arg Ala Xaa Asp Ile Thr
 115 120 125

Thr Ser Asp Arg Asp Xaa Xaa Lys Tyr Gly Xaa Leu Xaa Arg Leu Ala
 130 135 140

Val Glu Ala Gly Phe Asp Trp Val Tyr Tyr Glu Ser Xaa Xaa His Xaa
 145 150 155 160

His Xaa Ser Val Lys Xaa Xaa
 165

<210> 23

<211> 74

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: primer

<400> 23

gcgcgcttcg aagcgaggca gccagcgagg gagagagcga gcgggagcgc cggagcgagg 60

aaatcgatgc gcgc

74

<210> 24

<211> 74

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: primer

<400> 24

gcgcgcagat ctgggaaagc gcaagagaga gcgcacacgc acacacccgc cgcgcgact 60
 cgggatccgc gcgc 74

<210> 25
 <211> 996
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: gene
 activation construct

<400> 25
 cgaagcgagg cagccagcga gggagagagc gagcgggcga gccggagcga ggaaatcgaa 60
 ggttcgaatc cttccccac caccatcact ttcaaaagtc cgaaagaatc tgctccctgc 120
 ttgtgtgttg gaggtcgctg agtagtgccg gagtaaaatt taagctacaa caaggcaagg 180
 cttgaccgac aattgcatga agaatctgct taggggttagg cgttttgccc tgcttcgcga 240
 tgtacggggc agatatacgc gttgacattg attattgact agttattaat agtaatcaat 300
 tacgggggtca ttagttcata gcccatatat ggagttccgc gttacataac ttacggtaaa 360
 tggcccgccct ggctgaccgc ccaacgaccc ccgcccattg acgtcaataa tgacgtatgt 420
 tcccatagta acgccaatag ggactttcca ttgacgtcaa tgggtggact atttacggta 480
 aactgcccac ttggcagtac atcaagtgtg tcatatgccg agtacgcccc ctattgacgt 540
 caatgacggg aaatggcccg cctggcatta tgcccagtac atgaccttat gggactttcc 600
 tacttggcag tacatctacg tattagtcac cgctattacc atgggtgatgc gggtttggca 660
 gtacatcaat gggcgtggat agcgggtttga ctcacgggga tttccaagtc tccaccccat 720
 tgacgtcaat gggagtttgt tttggcacca aaatcaacgg gactttccaa aatgtcgtaa 780
 caactccgcc ccattgacgc aaatgggcgg taggcgtgta cgggtgggagg tctatataag 840
 cagagctctc tggctaacta gagaaccac tgcttactgg cttatcgaaa ttaatacgac 900
 tcactatagg gagaccaag cttggtaccg agctcggatc gatctgggaa agcgcaagag 960
 agagcgaca cgcacacacc cgccgcgcgc actcgg 996

<210> 26
 <211> 26
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: antisense
 construct

<400> 26
 gtcctggcgc cgccgccgcc gtcgcc 26

<210> 27
 <211> 26
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: antisense
 construct

<400> 27
 ttccgatgac cggcctttcg cggatga 26

<210> 28
 <211> 26
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: antisense
 construct

<400> 28
 gtgcacggaa aggtgcaggc cacact 26

<210> 29
 <211> 15
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: primer

<400> 29
 ggctccggta tgtgc 15

<210> 30
 <211> 15
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: primer

<400> 30
 ggggtacttc agggt 15

<210> 31
 <211> 25
 <212> DNA
 <213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: primer

<400> 31

cattggcagg aggagttgat tgtgg

25

<210> 32

<211> 25

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: primer

<400> 32

agcacctttt gaggaggatt tgggg

25